

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 13, 2003, 04:30:38 ; Search time 6675 Seconds
(without alignments)
9871.076 Million cell updates/sec

Title: US-09-918-485-1
Perfect score: 2711.
Sequence: 1 AGCTTCATAGAACTCAA.....GATCTAGATTGTCCTGCAG 2711

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST.*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estnu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_est3.*
12: gb_est4.*
13: gb_est5.*
14: gb_est6.*
15: em_estom.*
16: em_estom.*
17: em_ges_hum.*
18: em_ges_inv.*
19: em_ges_pin.*
20: em_ges_vrt.*
21: em_ges_fun.*
22: em_ges_mam.*
23: em_ges_mus.*
24: em_ges_pro.*
25: em_ges_rod.*
26: em_ges_pbg.*
27: em_ges_vrl.*
28: gb_ges1.*
29: gb_ges2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82.6	3.0	255	13	BQ280286
2	74.8	2.8	987	29	CNS014PQ
3	69.6	2.6	1148	13	BX360752
4	66.2	2.4	1200	13	BX415878

5	66.2	2.4	1200	13	BX437758
6	65.4	2.4	488	13	BX424122
7	64.6	2.4	1124	13	BX436282
8	64.4	2.4	994	13	BX414650
9	61.8	2.3	1101	29	CNS0106X
10	61.4	2.3	1101	29	CNS00EVL
11	60.6	2.2	637	29	CNS036CC
12	60.6	2.2	928	29	CNS00DKY
13	60.4	2.2	1076	13	BX338020
14	60.2	2.2	1101	29	CNS0039G
15	59.4	2.2	1200	13	BX415878
16	59	2.2	994	13	BX414650
17	58.8	2.2	1201	9	AL536104
18	58.6	2.2	1201	13	BX461824
19	58.4	2.2	1059	13	BX442829
20	58.2	2.1	1201	13	BX335665
21	58	2.1	1165	13	BX338369
22	57.8	2.1	938	29	CNS006TJ
23	57.8	2.1	1027	29	CNS02T50
24	57.6	2.1	1201	13	BX458623
25	57	2.1	1201	13	BX421282
26	56.8	2.1	660	28	BH183498
27	56.8	2.1	660	29	CNS070XJ
28	56.8	2.1	1001	29	CNS01400
29	56.8	2.1	1101	29	CNS001FB
30	56.8	2.1	1225	29	CNS0161D
31	56.4	2.1	973	29	CNS0080F
32	56.2	2.1	1201	9	AL532464
33	56.2	2.1	1201	13	BX437779
34	56	2.1	427	13	BX403499
35	56	2.1	1101	29	CNS00ESI
36	56	2.1	1200	13	BX437739
37	56	2.1	1201	13	BX461310
38	55.8	2.1	1101	29	CNS0100X
39	55.6	2.1	1201	9	AL556024
40	55.4	2.0	1101	29	CNS00Z38
41	55.2	2.0	1101	29	CNS004ZW
42	55.2	2.0	1101	29	CNS016LI
43	55	2.0	1101	29	CNS003BD
44	55	2.0	1200	13	BX436510
45	55	2.0	1201	13	BX458623

ALIGNMENTS

RESULT 1
BQ280286
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES

BQ280286
PAC000000001474 Pioneer AF-1 array Zea mays CDNA, mRNA sequence.
BQ280286
EST.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
Haben,J.
Analysis of gene expression in drought stressed maize
Unpublished
Contact: Haben J
Trait and Technology Development, Agronomic Traits
Pioneer Hi-Bred International, Inc.
7250 NW 62nd Ave., P.O. Box 552, Johnston, IA 50131-0552, USA
Tel: 515 270 4130
Fax: 515 334 4778
Email: jeffrey.haben@pioneer.com.
Location/Qualifiers
1..255
/organism="Zea mays"
/mol_type="mRNA"

[illegible]

RESULT 3	EST 05-MAY-2003
EX360752/c	
LOCUS	1148 bp
DEFINITION	linear mRNA
	EX360752 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
	clone CS021074V17 5-PRIME. mRNA sequence.

Clone CS0010/AY117 5'-PRIME: *homo sapiens* sequence.
 BX360752
 EX360752.1 GI: 30374469
 EST.
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1148)
 Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by life technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 10246.r for
 more information about this cluster, see
<http://www.genoscope.cns.fr/>
<http://cgi-bin/cluster.cgi?seq=CS001074CB090PI&cluster=10246.r>. Contact :
 Feng Liang Email : liang@lifetech.com URL : Corporation 1600
<http://fulllength.invitrogen.com/> Invitrogen
 Parady Avenue Genoscope sequence ID : CS001074CB09QPI.
 Location/Qualifiers
 1..1148
 FEATURES
 source

FEATURES	SOURCE
Location/Qualifiers	
1. 1148	
/organism="Homo sapiens"	
/mol_type="mRNA"	
/db_xref="taxon:9606"	
/clone="CS0D174YD17"	
/tissue_type="PLACENTA COT 25-NORMALIZED"	
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"	
/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT2 vector. Library was normalized."	
301 a 193 c 115 g 277 t	262 others
BASE COUNT	
ORIGIN	

	Query Match	2.4%	Score 69.6;	DB 13;	Length 1148;
Best Local Similarity	34.8%	Pred. No. 0.019;			
Matches 199;	Conservative	90;	Mismatches 282;	Indels 1;	Gaps 1
Qy	39	TCCTTTTAAATCTCTCTACTCTACAGGSGGTAGAACATATCGGTGCTANTTTTAAATATGG	98		
Db	1014	TTTTTAATTTTAAATATTTATTAATAAATKKGGAAGAATAAAGAKDTTAAAKAATKDKTKK	955		

Wed Oct 15 11:56:16 2003

BASE COUNT	ORIGIN	47 a	33 c	65 g	50 t	Score 82.6; DB 13; Length 255;	3 0k; Best Local Similarity 59.7k; Pred. No. 0.0001;	Mismatches 0; Matches 94; Indels 0; Gaps 0;
QY	259	RATCAATGCATACCTTCAATATCTGTTTAAAGTAAATCCCTGAAGAAGTACTTTTGGATCGGAAA	318					
Db	22	AACGAGTGCATCCCGTACAACTCCCTCTCCAAACCGGAGGTGGAGGTGCTCGCGCGCGAG	81					
QY	319	CGGATATCAACTGTAATTAATCAATGTGATATTTCTCTGTCACTTGTTCAGTTTTCGTGTA	378					
Db	82	CGCATTCGAGACCGGCTACACCCCGATTCGACATCTCCCTCTCCCTACCCAGTTTCCTCCTC	141					
QY	379	TCTTAACATTTGTACCAAGGGGAGAGATTTTTAGTTCGGATTAATAGATTTTTGTATGGGGAATA	438					
Db	142	TCGAGATTTCTGTCGACGGCGCGGCTTCGTGCTCGGCCCTCGTGACATCATCTATGGGGCATC	201					
QY	439	GTTCGCCCTTCTCAATGGGATGCATTTCTTAGTAGCAAAATGGAACAATTAATAA	491					
Db	202	TTGCGCCCGCTCCAGTGTGGGACGCTTCTTCGTGCGAGATCGACAGTAAATAA	254					

RESULT 2	CNS014PQ/c
LOCUS	Drosophila melanogaster genome survey sequence Sp6 end of BAC BACN1222 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
DEFINITION	
VERSION	AL10456
FEATURES	AL10456.1 GI:5616067
KEYWORDS	GSS:
SOURCE	Drosophila melanogaster (fruit fly)
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Phlebotomidae; Drosophilidae; Drosophila. 1 (bases 1 to 987) Genoscope.
REFERENCE	Direct Submission
AUTHORS	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
TITLE	BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
JOURNAL	- Web : www.genoscope.cns.fr)

Web : www.genosciences.fr
Determination of the BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
<http://beta1/www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaut at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBeloBAC11.

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FEATURES
source
location Location/Qualifiers
1..987
organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
clone="BACN12P22"
clone_lib="DrosBAC"
plasmid="pBelOBAC11"
/notes="end : SP6"
257 a 122 g 241 t 245 others
BASE COUNT

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[illegible]

Qy	99	GGCATAATATGTAATTTTATATAAAATTTGTTCAGTTTTTTTGTATATTTTTTCATGAAGATGCT	158
Db	954	ATDKKAKAKATAAAAKWTTKTTTAAANWTTTTKTKATWTTTKTTATTATDTDKAAAKKTKTW	895
Qy	159	CATATGTATTAAATCGTCGTATGAAGAAACAGCATATCAAACTATCAGAACTTTGGTAGTTT	218
Db	894	ATTTTAAAKTTATTATATAAARATGAAAGARAAATTAATAKATAKKGATWTTTTKAATTK	835
Qy	219	AATAAAAAACGGAGGTATTTTATCGAGGAAAAATAATCAAAATCAATGCATACCTTTACAA	278
Db	834	KATAATKTKTKAWAAAKDTKWTAAKTKKATTAATTTTAAATKAAKAKAADAATDTATTK	775
Qy	279	TGTTTAAAGTAATCCTGAAGAAGTACTTTTGGATGGAGAACGGATATCAACTGGTAATTA	338
Db	774	KAAATKAKAAAAAKWKAASKA-TKKTATKTKAKKKKAAAGKKAATTAATTTTAAAAAAA	716
Qy	339	CTCAATTCGATATTTCTCTGTCACCTTGTTCAGTTTCTGGTATCTAACTTTGTACCGAGGGG	398
Db	715	AAAAAATTTTKTTTTTTTTTAAAAAATTTATTTTTATAAATTTAATWTTTTCATATATAATKWTWT	656
Qy	399	AGGATTTTTTAGTTCGATTAATAGATTTTGTATGGGGAATAGTTGGCCCTTCTCAATGGGA	458
Db	655	TTAAAGTATGTGAATGGKAAATGGTTTMMKMMMGTKTHTMTMMKGTWMTTGMAMAKTT	596
Qy	459	TGCATTTCTAGTACAAATTTGAACAATTAATTAATGAAGAAATAGCTGAAATTTGCTAGGAA	518
Db	595	KTMGKTKKMAATWKAATTTGHAAGAAAGTTATKTGRGAATAGAGAGATAAATTTATWMMGG	536
Qy	519	TGCTGCTATTGCTAATTTAGAGGAATTAGGAACAAATTTCAATATATATGTGGAAGCATT	578
Db	535	MGGHAMMGKMMMATGTGTTTKMAATTAGWTAGGGAGGAATAAKTTTAGATTATTGAGW	476
Qy	579	TAAAGAATGGGAAGAAGATCCATAAATCCAG	610
Db	475	TTATGATAAGGGGATGATTCGGATTTATGGAG	444

RESULT 4	EX415878	1200 bp	linear	EST 15-MAY-2003
LOCUS	EX415878			
DEFINITION	BX415878 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP008YI04			
ACCESSION	5-PRIME, mRNA	sequence.		
VERSION	EX415878			
KEYWORDS	EX415878.1	GI:30765550		
SOURCE	EST.			
ORGANISM	Homo sapiens (human)			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 1200)			
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.			
TITLE	Full-length cDNA libraries and normalization			

FEATURES
source

EX437758	EX437758	1200 bp	mRNA	linear	EST 15-MAY-2003
LOCUS	EX437758	1200 bp	Hom sapiens	Thymus	Hom sapiens
DEFINITION	5-PRIME, mRNA sequence.				
ACCESSION	EX437758				
VERSION	EX437758.1	GI:30773605			
KEYWORDS	EST.				
SOURCE	Hom sapiens (human)				
ORGANISM	Hom sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				


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RESULT 7
BX436282      1124 bp mRNA linear EST 15-MAY-2003
LOCUS
DEFINITION    BX436282 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP001YC01
5-PRIME, mRNA sequence.
ACCESSION     BX436282
VERSION       BX436282.1 GI:30787521
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 1124)
AUTHORS       Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE         Full-length cDNA libraries and normalization
JOURNAL       Unpublished
COMMENT       Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0CAP001AB01QPI.

FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT    129 a 29 c 109 g 435 t 422 others
ORIGIN
Query Match      2.4%; Score 64.6; DB 13; Length 1124;
Best Local Similarity 23.3%; Pred. No. 0.15;
Matches 115; Conservative 160; Mismatches 218; Indels 0; Gaps 0;

QY 87 TTTTAAATATGCGGCATATATGATATTTTATAAAATTTGTTACGTTTTTGTATTTTTT 146
DB 464 TTTTTRRRRRRTTTTDDTDRRRTTTRTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 523

QY 147 CATAAGATGTCATATGATTAATAATCGTGGTAAATGAAACAGTATCAAACTATCAGAA 206
DB 524 TTTTDDTDRRRRRRRRTTTTDDTDRRRTTTRTTTTTTTTTTTTTTTTTTTTTTTTT 583

QY 207 CTTTGTAGTTTATAAAAAACGGAGGTATTTTATGAGGAGAAATAATCAAAATCAATG 266
DB 584 RKTDRDTTTRRRRRRRRRRTTDRRRRTTTRTTTTTTTTTTTTTTTTTTTTTTTTT 643

QY 267 CATACCTTCAATTTGTTTAAAGTAATCTGAAGAAGTACTTTTGGATGGAGAACGGATATC 326
DB 644 RDTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 703

QY 327 AACTGGTAATCTCAATGATATTTCTCTGTCACCTGTGTTTCTGTTCTGATCTAACTT 386
DB 704 RDTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 763

QY 387 TGTACACGGGGAGGAGTTTGTAGTGAATTAATAGATTTTGTATGGGATAGTTGGCCC 446
DB 764 TRRRRTTTRRRRRRTTTRRRRTTTRTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 823

QY 447 TTCTCAATGGGATCTTCTAGTACAAATTAATTAATTAATTAATTAATTAATTAATTAAT 506
DB 824 TTTTTRRRRRRRRTTTRTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 883

QY 507 ATTTGCTAGGAATGCTGCTATTGCTAATTTAGAAGGATTAGGAAACAATTTCAATATATA 566

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884 RRDDTTTTTTTDTTDTTDTTDTTDTTDTTDTTDTTDTTDTTDTTDTTDTTDTTDTTDTT 943
QY 567 TGTGGAAGCATTT 579
DB 944 TDRRRRRRTTTT 956

RESULT 8
BX414650/c
LOCUS
DEFINITION    BX414650 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP001YN02
3-PRIME, mRNA sequence.
ACCESSION     BX414650
VERSION       BX414650.1 GI:30763455
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 994)
AUTHORS       Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE         Full-length cDNA libraries and normalization
JOURNAL       Unpublished
COMMENT       Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6015.f
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0CAP001DG01NPI.

FEATURES
source
Location/Qualifiers
1..994
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP001YN02"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT    185 a 121 c 25 g 324 t 339 others
ORIGIN
Query Match      2.4%; Score 64.4; DB 13; Length 994;
Best Local Similarity 22.4%; Pred. No. 0.17;
Matches 120; Conservative 184; Mismatches 227; Indels 4; Gaps 1;

QY 71 GAACATAATCGGTCAATTTTAAATATGCGGCATATATGATATTTTATAAAATTTGTTAC 130
DB 906 GDDWDWDTATWAAADWAAWAAATWTTDWTATWTRKDKATWKADDDDDAKTKTT 847

QY 131 GTTTTGTATTTTTCATAGATGTGTCATATGATTAATAATCGGTGATGAAACAG 190
DB 846 TTTTWWKAWTDWAGTAKWADATWADAADAWAAWAAWAAWAAWAAWAAWAAWAAW 787

QY 191 TATCAACTATCAGAACTTTGTAGTTTAAATAAAAAACGGAGGTATTTTATGGAGAAA 250
DB 786 WWWNDWADAAWAAWADTKDKAWRAADWAAWAAWAAWAAWAAWAAWAAWAAWAAW 727

QY 251 ATAATCAAAATCAATGCATACCTTACAATTTGTTAAAGTAATCTGAAGAAGTACTTTG 310
DB 726 DGAGGRDKDRDWAARWDDADAAAARAAAATAWATWTKWKKDKDWAATAWDTAKG 667

QY 311 ATGGAGACGGATATCACTGTTAATTAATCAATGATTTCTCTGCTCACTTGTTCACT 370
DB 666 RKDDARDWAAWAAWTTTTTTTTTTTAAWAADKAWKWKATATTTTTTTTTTTTTTTT 607

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The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammose in Peter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

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source
1. .1101
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/db_xref="taxon:7227"
/clone="BACR08K10"
/tissue_lib="RPCL-98"
/note="end : TET3"

BASE COUNT      201 a      64 c      131 g      202 t      503 others
ORIGIN

Query Match      2.2%; Score 60.2; DB 29; Length 1101;
Best Local Similarity 17.0%; Pred. No. 0.94;
Matches 119; Conservative 297; Mismatches 283; Indels 2; Gaps 2;

QY 1890 AGATATGCTCTTCAGAAACTATGCAATAGGGAGAACTTAACATCTAGAACATTTAG 1949
Db 1096 WGGDTTWDRTDKDDWMTKWTWKKDRADRWAGDADRWADWDDGAGTTTATWMMWMM 1037
QY 1950 ATATACCGATTTTAGTAACTCTTTTCATTAGAGCTAATCAGATATATTTGGGATAG 2009
Db 1036 WATWDTWBDKWWATAAATATWTTWRTAWRADWAGRDGAGKDRDADTADGAGRD 977
QY 2010 TGACAACTCTATTGGTGGAGGTTCTATTAGTAGGTTGAACTTTATATAGATAAAT 2069
Db 976 GGRKRDKDKRDGDDKGGKKAKAATWATWMDWMDWMDKMDKMDGAKDRKADDD 917
QY 2070 TGAATATTTCTAGACAGTCAACATTTGACAGCAATCTGATTAGAAAGACCAAA 2129
Db 916 GAGDKDDGKADDDTGTGKDDDKDKWDDWAKGTWGDATWAAATDWWGWA 857
QY 2130 GCGGTGTAATGCTGTTTACTTCTTCAATCAATCGGGTAAACACCGATGTGACGA 2189
Db 856 DWWTDAAADWADWADWADWADWADWADWADWADWADWADWADWADWADWADWAD 798
QY 2190 TTATCATATGATCAAGTATCAATTTAGTGGATTTGTTATCAGATGAATTTGTCTGA 2249
Db 797 ADDKRDADDDDAATTTTTRDTDDWKTDTWTRWAADRTWDRDDDDDRDRAGT 738
QY 2250 TCAAAAGCGAGAAATGTCGAGAAAGTCAAAATCGAAGCACTCAGTGTACGCGGA- 2308
Db 737 AGKWRRTWKRWRKRDTRWDADDDTARDRRRGDDGADGKGTGKRRRRDRAT 678
QY 2309 ATTTACTTCAAGATCAAACTTTCAGAGGATCAATAGACCAACAGACCGTGGCTCGAG 2368
Db 677 WERTDAWADAADWTTTDDTDWDRKDRRRRTTARAADWTTWKAADWADWADWAD 618
QY 2369 GAAGTACAGATATTCACATCCAGAGGAGATGACGTATTCACAGAGAAATTCAGTCA 2428
Db 617 WKTRADRWDAADTWDADKADRDWAKARAWARRDRARAARADRRWTTTGGTTATWT 558
QY 2429 TACCGGTACCGTTCAGTGTCTATCCAACTATTTATATCAGAAATAGATGATGCGA 2488
Db 557 TWAARAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAW 498
QY 2489 AATTAAGACTTATACCCGTTATGAATTAAGAGGGGTATATCAAGATAGTCAAGACTT 2548
Db 497 TAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAW 438
QY 2549 AATCTATTTGATCGGTACATCAATGCAAAACACGAAATAGTA 2589

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Db 437 WTTTWTAAATTTATTTTWTATAAAAAAAMWMTWTATA 397

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RESULT 15

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BX415878/c
BX415878/c
LOCUS
DEFINITION
BX415878 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP008Y104
5-PRIME, mRNA sequence.
ACCESSION
BX415878
VERSION
BX415878.1 GI:30765550
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1200)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0CAP008BE02QF1.
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/clone="CS0CAP008Y104"
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/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT      428 a      70 c      85 g      447 t
ORIGIN

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Query Match      2.2%; Score 59.4; DB 13; Length 1200;
Best Local Similarity 38.9%; Pred. No. 1.3;
Matches 204; Conservative 67; Mismatches 246; Indels 8; Gaps 3;

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QY 145 TTCATAGATGTGTCAATGATTAATTAATCGGTGTAATGAAACAGTATCAAACTATCAG 204
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QY 205 AACTTTGTCTGTAAATAAAACCGAGGTATTTTATGGAGGAAATAATCAAAATCAA 264
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QY 265 TGCATACCTTCAACAATTTGTTTAAAGTAATCTCTGAAGAGTACTTTTGGATGGAGACG 324
Db 839 TTTTWTAAATTTAAWTTTAAWTTTAAWTTTAAWTTTAAWTTTAAWTTTAAWTTTAA 782
QY 325 TCAACTGGTAATTAATCAATGATTAATTTCTCTGTCACCTTGTTCAGTTCTGTGATCTAAC 384
Db 781 TAAWTTATATTTTATGHTATATATATATATATATATATATATATATATATATATAT 722
QY 385 TTTGTACACGCGGGGAGGATTTTGTAGTGAATATAGATTTTGTATGGGGAATAGTTCGC 444
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us-09-918-485-1.rst

Wed Oct 15 11:56:16 2003

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Qy 561 TATATATGTTGAAGCATTTAAAGATGGAAGAGATCCTAATAA 605
Db 541 AATTTWATTAATAAAATTTWAAWWTATWAAWTTTAAAAATTA 497

Search completed: October 13, 2003, 10:12:43
Job time : 6683 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 13, 2003, 08:21:18 ; Search time 2257 Seconds
(without alignments)
3116.763 Million cell updates/sec

Title: US-09-918-485-1

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Gapop 10.0 , Gapext 1.0

Searched: 1731049 seqs, 1297405648 residues

Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	2419.8	89.3	3567	11	US-09-972-175-58
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23 1071.8 39.5 3531 9 US-09-873-873-11
24 1071.8 39.5 3531 9 US-09-873-873-13
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27 1071.8 39.5 3531 11 US-09-997-914-13
28 1071.8 39.5 3531 12 US-10-365-645-9
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ALIGNMENTS

RESULT 1

US-09-918-485-1

; Sequence 1, Application US/09918485

; Publication No. US20030115628A1

; GENERAL INFORMATION:

; APPLICANT: SANCHIS, Vincent

; LERECUS, Didier

; MENOU, Ghislaine

; LECADRET, Marguerite-Marie

; MARTOURET, Daniel

; DEDONDER, Raymond

; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR

; POLYPEPTIDES ENDOWED WITH A LARVICIDAL ACTIVITY TOWARDS

; LEPIDOPTERA

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: USA

; ZIP: 22313

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/918,485

; FILING DATE: 25-Oct-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/461,551

; FILING DATE: 05-JUN-1995

; APPLICATION NUMBER: US 08/251,652

; FILING DATE: 31-MAY-1994

; APPLICATION NUMBER: US 07/458,754

; FILING DATE: 11-DEC-1989

; APPLICATION NUMBER: EP 88 401 121.4

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RESULT 2

US-09-972-175-1

Sequence 1, Application US/09972175

Publication No. US20030101482A1

GENERAL INFORMATION:

APPLICANT: Baum, James A.

Gilmer, Amy Jelen

Mettus, Anne-Marie Light

TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS

NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,175
FILING DATE: 05-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/337,635
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3567
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-972-175-1

Query Match 89.6%; Score 2429.4; DB 11; Length 3567;
Best Local Similarity 98.9%; Pred. No. 0; Mismatches 26; Indels 0; Gaps 0;
Matches 2445; Conservative 0;

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Db 1 ATGGAGGAAAAATTAACAAATCAATGCATACCTTCAATTTGTTAAAGTAATCCTGAAGAA 60
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Db 181 GATTTGTTATGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTTGAA 240
Qy 481 CAATTAATTAATGAAGAATAGCTGAATTTGCTAGGAATGCTGCTATTGCTAATTTAGAA 540
Db 241 CAATTAATTAATGAAGAATAGCTGAATTTGCTAGGAATGCTGCTATTGCTAATTTAGAA 300
Qy 541 GGATTAGGAACAATTTCAATATATATGTTGGAAGCATTTAAAGATGGGAAGATCCT 600
Db 301 GGATTAGGAACAATTTCAATATATATGTTGGAAGCATTTAAAGATGGGAAGATCCT 360
Qy 601 AATATCCAGCAACCCAGGACAGAGTAATTAATGCTTTTGTATATCTTGTATGCGGTACTT 660
Db 361 AATATCCAGCAACCCAGGACAGAGTAATTAATGCTTTTGTATATCTTGTATGCGGTACTT 420
Qy 661 GAAAGGACATTCCTTCGTTTTCGAATTTCTGGAATTTGAAGTACCCCTTTTATCCGTTTAT 720

Db 421 GAAAGGACATTCCTCGTTGGCAATTTCTGGATTTGAGTACCCCTTTTATCGTTTAT 480
Qy 721 GCTCAAGCGGCAATCTGCAATCTAGCTATATTAAGATTCGTGTAATTTTGGGAAGA 780
Db 481 GCTCAAGCGGCAATCTGCAATCTAGCTATATTAAGATTCGTGTAATTTTGGGAAGA 540
Qy 781 TTGGGATTCACAGCAATAATGTCAATGAAACCTATATAGACTAATTAGGCATATTGAT 840
Db 541 TGCGGATTCACACGATAAATGTCAATGAAACCTATATAGACTAATTAGGCATATTGAT 600
Qy 841 GAATATGCTGATCACTGTGCAAAATACGTATATCGGGGATTAATAATTTACCGAAATCT 900
Db 601 GAATATGCTGATCACTGTGCAAAATACGTATATCGGGGATTAATAATTTACCGAAATCT 660
Qy 901 ACGTATCAAGATTTGGATAACATATATCGATTTACGGAGACTTAACTGACTGTATTA 960
Db 661 ACGTATCAAGATTTGGATAACATATATCGATTTACGGAGACTTAACTGACTGTATTA 720
Qy 961 GATATCGCGCTTCTTTCCAACTATGACAAATAGAGATATCAAATTCAGCCAGTTGGT 1020
Db 721 GATATCGCGCTTCTTTCCAACTATGACAAATAGAGATATCAAATTCAGCCAGTTGGT 780
Qy 1021 CAACTAACAGGAGATTTATAGGACCCATTAATTAATTTTAAATCCACAGTTACAGTCT 1080
Db 781 CAACTAACAGGAGATTTATAGGACCCATTAATTAATTTTAAATCCACAGTTACAGTCT 840
Qy 1081 GTAGCTCAATACCTACTTTTAACTGATGAGAGCGACGCAATTAAGAATCCTCATTTA 1140
Db 841 GTAGCTCAATACCTACTTTTAACTGATGAGAGCGACGCAATTAAGAATCCTCATTTA 900
Qy 1141 TTTGATATATGATTAATCTTAAGATTTTACGGATTTAGGATTTAGTGTGAGCGCAATTT 1200
Db 901 TTTGATATATGATTAATCTTAAGATTTTACGGATTTAGGATTTAGTGTGAGCGCAATTT 960
Qy 1201 TATTGGGAGGACATCGAGTAAATCTAGCTTTATAGAGGTGTGACATACATCTCCT 1260
Db 961 TATTGGGAGGACATCGAGTAAATCTAGCTTTATAGAGGTGTGACATACATCTCCT 1020
Qy 1261 ATATATGGAAGAGAGCGCAACAGGAGCTTCAAGATCTTTTAACTGAGGATTAAGTGTGCGTA 1320
Db 1021 ATATATGGAAGAGAGCGCAACAGGAGCTTCAAGATCTTTTAACTGAGGATTAAGTGTGCGTA 1080
Qy 1321 TTTAGGACTTTATCAATTCCTACTTTACGATTTATACGAACTTCCAGGCGCCACAT 1380
Db 1081 TTTAGGACTTTATCAATTCCTACTTTACGATTTATACGAACTTCCAGGCGCCACCA 1140
Qy 1381 TTTAATTTTACGTTGGTGAAGGAGTAGAATTTTACACCTTACAAATAGCTTTTACGTAT 1440
Db 1141 TTTAATTTTACGTTGGTGAAGGAGTAGAATTTTACACCTTACAAATAGCTTTTACGTAT 1200
Qy 1441 GCAGGAAGAGTACGGTTGATTTCTTTAACTGAATTTACCGCTGAGGATTAATAGTGTGCGA 1500
Db 1201 CGAGGAAGAGTACGGTTGATTTCTTTAACTGAATTTACCGCTGAGGATTAATAGTGTGCGA 1260
Qy 1501 CCTCGGAAGGATATAGTCACTGTTTATGTCATGCAACTTTTGTTCAGAGATCTGGAACA 1560
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Qy 1621 ACATTTGATCAGAGAGATTAATCAATATCTTTTGTGAAAGGATTTAGAGTTTGGGG 1680
Db 1381 ACATTTGATCAGAGAGATTAATCAATATCTTTTGTGAAAGGATTTAGAGTTTGGGG 1440
Qy 1681 GGCACCTCTGCTATTAACAGGACGAGATTTACAGGAGGATATCTTCCGAAGAAATACC 1740
Db 1441 GGCACCTCTGCTATTAACAGGACGAGATTTACAGGAGGATATCTTCCGAAGAAATACC 1500
Qy 1741 TTTGGGATTTTGTATCTCTACAGTCAATATTAATTCACCAATTAACCAAGATACCGT 1800
Db 1501 TTTGGGATTTTGTATCTCTACAGTCAATATTAATTCACCAATTAACCAAGATACCGT 1560

Qy 1801 TTAAGATTTCTGTACGCTTCCAGTAGGAGTCAGCAGTTTATAGTATTAACAGAGCGGCA 1860
Db 1561 TTAAGATTTCTGTACGCTTCCAGTAGGAGTCAGCAGTTTATAGTATTAACAGAGCGGCA 1620
Qy 1861 TCCACAGGAGTGGGAGGCCCAAGTTAGTGTAGATATCCCTCTTTCAGAAAACTATGGAAATA 1920
Db 1621 TCCACAGGAGTGGGAGGCCCAAGTTAGTGTAAATATGCTCTTTCAGAAAACTATGGAAATA 1680
Qy 1921 GGGGAGAACTTTAACATCTAGAACATTTAGATATATACCGATTTTAGTAATCTCTTTTCAATTT 1980
Db 1681 GGGGAGAACTTTAACATCTAGAACATTTAGATATATACCGATTTTAGTAATCTCTTTTCAATTT 1740
Qy 1981 AGAGCTAATCCAGATATATTTGGGATAAGTGAACCACTCTATTTTGGTGACAGTTCTTAT 2040
Db 1741 AGAGCTAATCCAGATATATTTGGGATAAGTGAACCACTCTATTTTGGTGACAGTTCTTAT 1800
Qy 2041 AGTAGCGTGAATTTTATATAGTAAATTCGAATTTTCTAGCAGATGCAACATTTGAA 2100
Db 1801 AGTAGCGTGAATTTTATATAGTAAATTCGAATTTTCTAGCAGATGCAACATTTGAA 1860
Qy 2101 GCAGAACTCTGATTTTGAAGAGCAACAAAGCGGTGAATGCCCTGTCTTCTTCCAAT 2160
Db 1861 GCAGAACTCTGATTTTGAAGAGCAACAAAGCGGTGAATGCCCTGTCTTCTTCCAAT 1920
Qy 2161 CAAATCGGTTAAAAACCGATGTGAGCGATTTATCATTTGATTCAGTATCCAAATTTAGTG 2220
Db 1921 CAAATCGGTTAAAAACCGATGTGAGCGATTTATCATTTGATTCAGTATCCAAATTTAGTG 1980
Qy 2221 GATTGTTTATCAGATGAATTTTCTGTGGATGAAAGCGAGATTTGTCCGAGAAAGTCAAA 2280
Db 1981 GATTGTTTATCAGATGAATTTTCTGTGGATGAAAGCGAGATTTGTCCGAGAAAGTCAAA 2040
Qy 2281 CATGCGAAGCGACTCAGTGTAGCGGAAATTTTACTTCAAGATCCAACTTTCAGAGGATC 2340
Db 2041 CATGCGAAGCGACTCAGTGTAGCGGAAATTTTACTTCAAGATCCAACTTTCAGAGGATC 2100
Qy 2341 AATAGACAACAGACCGGTGGAGAGGAGTACAGATATACCAATCCAGAGGAGAT 2400
Db 2101 AATAGACAACAGACCGGTGGAGAGGAGTACAGATATACCAATCCAGAGGAGAT 2160
Qy 2401 GACGTTTCAAAAGAGAAATTTACGTACACTACCGGTACCGTTGATGAGTGTCTATCCAAAG 2460
Db 2161 GACGTTTCAAAAGAGAAATTTACGTACACTACCGGTACCGTTGATGAGTGTCTATCCAAAG 2220
Qy 2461 TATTTATATCAGAAATATAGATGAGTGAATTTAAAGCTTATACCGCTTATGAATTAAGA 2520
Db 2221 TATTTATATCAGAAATATAGATGAGTGAATTTAAAGCTTATACCGCTTATGAATTAAGA 2280
Qy 2521 GGSTATATCGAAGATAGTCAAGACTTAGAAATCTTATTTGATCGGTACAAATGCAAAACAC 2580
Db 2281 GGSTATATCGAAGATAGTCAAGACTTAGAAATCTTATTTGATCGGTACAAATGCAAAACAC 2340
Qy 2581 GAATAGTAAATGTCAGGACCGGTTCCTTATGCGCTTTCAGCCCAAAAGTCCAATC 2640
Db 2341 GAATAGTAAATGTCAGGACCGGTTCCTTATGCGCTTTCAGCCCAAAAGTCCAATC 2400
Qy 2641 GAAAGTGTGGAGAACCGAATCGATGCGGCCACACCTTTGAATCTGATCTAGAT 2700
Db 2401 GAAAGTGTGGAGAACCGAATCGATGCGGCCACACCTTTGAATCTGATCTAGAT 2460
Qy 2701 TGTTCCTGCGAG 2711
Db 2461 TGTTCCTGCGAG 2471

RESULT 3
US-09-972-175-11
; Sequence 11, Application US/09972175
; Publication No. US20030101482A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; Gilmer, Amy Jelen

601 AATAATCCAGCACACAGGACAGAGTAATGTATCGCTTTCGTATACCTTGATGGGCTACTT 660
361 AATAATCCAGCACACAGGACAGAGTAATGTATCGCTTTCGTATACCTTGATGGGCTACTT 420
661 GAAAGGGACATCTCTTTCGTTTCGAAATTCCTGGATTTGAAGTACCCCTTTTATCCGTTTAT 720
421 GAAAGGGACATCTCTTTCGTTTCGAAATTCCTGGATTTGAAGTACCCCTTTTATCCGTTTAT 480
721 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTCGTATAATTTTGGAGAAAGA 780
481 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTCGTATAATTTTGGAGAAAGA 540
781 TTGGGATTCACACAGTAATGTCAATGAATACTAATAGACTAATAGGCAATATTGAT 840
541 TTGGGATTCACACAGTAATGTCAATGAATACTAATAGACTAATAGGCAATATTGAT 600
841 GAATATGCTGATCAGCTGTCMAATACGTATAATTCGGGGATTAATAATTTTACCGAATCT 900
601 GAATATGCTGATCAGCTGTCMAATACGTATAATTCGGGGATTAATAATTTTACCGAATCT 660
901 ACGTATCAAGATTTGGATAACATATAATCGATTACGGAGAGACTTAACATTTGACTGTATTA 960
661 ACGTATCAAGATTTGGATAACATATAATCGATTACGGAGAGACTTAACATTTGACTGTATTA 720
961 GATATCGCGCTTCTTTTCCAACTATGACATAGAGATATCCAAATTCAGCCAGTTGGT 1020
721 GATATCGCGCTTCTTTTCCAACTATGACATAGAGATATCCAAATTCAGCCAGTTGGT 780
1021 CAACTAAAGGAGAGCTTTATACGGACCAATTAATTTTAAATCCACAGTTACAGTCT 1080
781 CAACTAAAGGAGAGCTTTATACGGACCAATTAATTTTAAATCCACAGTTACAGTCT 840
1081 GTAGCTCAATTCCTACTTTTAAAGGTTATGGAGAGCAGCGCAATTAGAATCTCTCATTTA 1140
841 GTAGCTCAATTCCTACTTTTAAAGGTTATGGAGAGCAGCGCAATTAGAATCTCTCATTTA 900
1141 TTTGATATTAATTAATCTTACAACTTTTACGGATTTGTTAGTTGGAGCGCAATTTT 1200
901 TTTGATATTAATTAATCTTACAACTTTTACGGATTTGTTAGTTGGAGCGCAATTTT 960
1201 TATTGGGAGGACATCGAGTAATATCTAGCTTTATAGGAGTGGTAACATACTCTCT 1260
961 TATTGGGAGGACATCGAGTAATATCTAGCTTTATAGGAGTGGTAACATACTCTCT 1020
1261 ATATATGGAAGAGAGCGCAACAGGAGCTTCAAGATCTTTTAAATGGACCGGTA 1320
1021 ATATATGGAAGAGAGCGCAACAGGAGCTTCAAGATCTTTTAAATGGACCGGTA 1080
1321 TTTAGACTTTTATCAATTCCTTATCGATTTATACGAAACCTTGGCAGCGCCACCAT 1380
1081 TTTAGACTTTTATCAATTCCTTATCGATTTATACGAAACCTTGGCAGCGCCACCA 1140
1381 TTTAATTTACGTTGGTGAAGAGTAGAATTTCTTACACCTTACAAATAGCTTTACGTAT 1440
1141 TTTAATTTACGTTGGTGAAGAGTAGAATTTCTTACACCTTACAAATAGCTTTACGTAT 1200
1441 GCAGGAAGAGGTACGGTTGATTTCTTAACTGAATTAACCGCTTGAGGATAATAGTGCCA 1500
1201 GCAGGAAGAGGTACGGTTGATTTCTTAACTGAATTAACCGCTTGAGGATAATAGTGCCA 1260
1501 CCTCGGAAGAGATATAGTCAATCGTTTATGTCATGCAATTTTGGTCAAGATCTGGAACA 1560
1261 CCTCGGAAGAGATATAGTCAATCGTTTATGTCATGCAATTTTGGTCAAGATCTGGAACA 1320
1561 CCTTTTAACTGTTGAGTATTTCTTGGACGATCTGAGTGCACCTCTTCAAT 1620
1321 CCTTTTAACTGTTGAGTATTTCTTGGACGATCTGAGTGCACCTCTTCAAT 1380
1621 ACAATTTGATCCAGAGAGATTAATCAATACCTTTTGTGAAAGGATTTAGAGTTTGGGG 1680
1381 ACAATTTGATCCAGAGAGATTAATCAATACCTTTTGTGAAAGGATTTAGAGTTTGGGG 1440
1681 GGCACCTCTGTCTATTAAGGACAGGATTTTACAGGAGGGATATCTTTCGAAGAAATACC 1740

RESULT 5

1441 GGCACCTCTGTCTATTACAGGACAGGATTTACAGGAGGGGATATCTTCCGAAGAAATACC 1500
1741 TTTTGGTGAATTTTGTATCTCTCAAGTCAATATTAATTTACCAATTTACCCAAAGATACCGT 1800
1501 TTTTGGTGAATTTTGTATCTCTCAAGTCAATATTAATTTACCAATTTACCCAAAGATACCGT 1560
1801 TTAAGATTTTGGTACGCTTCCAGTAGGATGACAGCATTTATAGTATTAACAGAGCGGCA 1860
1561 TTAAGATTTTGGTACGCTTCCAGTAGGATGACAGCATTTATAGTATTAACAGAGCGGCA 1620
1861 TCCACAGAGTGGGAGGCCAAGTTAGTAGATATGCCTCTTTCAGAAAATCTATGGAATA 1920
1621 TCCACAGAGTGGGAGGCCAAGTTAGTAGATATGCCTCTTTCAGAAAATCTATGGAATA 1680
1921 GGGGAGAACTTAACTCTAGAACATTTAGATATACCGATTTTAGTAAATCTCTTTTCTATTT 1980
1681 GGGGAGAACTTAACTCTAGAACATTTAGATATACCGATTTTAGTAAATCTCTTTTCTATTT 1740
1981 AGAGCTAATCCAGATATATAATTTGGGATTAAGTGAACAACTCTATTTTGGTGCAGGTTCTAT 2040
1741 AGAGCTAATCCAGATATATAATTTGGGATTAAGTGAACAACTCTATTTTGGTGCAGGTTCTAT 1800
2041 AGTAGCGTTGAATTTATATAGATATAATTTGAAATTTATTTCTAGCAGATGCAACATTTGAA 2100
1801 AGTAGCGTTGAATTTATATAGATATAATTTGAAATTTATTTCTAGCAGATGCAACATTTGAA 1860
2101 CGAGAACTCTGATTTAGAAAGACACAAAGGCGGTGAATGCGCTGTTTACTTCTTCCAAAT 2160
1861 GCGAATCTGATTTAGAAAGACACAAAGGCGGTGAATGCGCTGTTTACTTCTTCCAAAT 1920
2161 CAAATCGGTTTAAACCCGATGTGACGATTTATCATATTTGATCAAGTATCCAAATTTAGTG 2220
1921 CAAATCGGTTTAAACCCGATGTGACGATTTATCATATTTGATCAAGTATCCAAATTTAGTG 1980
2221 GATTTGTTTATCAGATGAATTTTGTCTGGATGAAGACGAGAAATTTGTCCGAGAAAGTCAAA 2280
1981 GATTTGTTTATCAGATGAATTTTGTCTGGATGAAGACGAGAAATTTGTCCGAGAAAGTCAAA 2040
2281 CATGCGAAGCGACTCAGTGATGAGCGGAAATTTTACTTCAAGTCCAAACTTTCAGAGGGATC 2340
2041 CATGCGAAGCGACTCAGTGATGAGCGGAAATTTTACTTCAAGTCCAAACTTTCAGAGGGATC 2100
2341 AATAGAACACAGACCGTGGCTGGAGAGAGTACAGATTTTACCATCCAAAGAGAGAT 2400
2101 AATAGAACACAGACCGTGGCTGGAGAGAGTACAGATTTTACCATCCAAAGAGAGAT 2160
2401 GACGATTTCAAAGAGAAATTAAGTCACTACCGGTACCGTTGATGAGTGTATCCAAAG 2460
2161 GACGATTTCAAAGAGAAATTAAGTCACTACCGGTACCGTTGATGAGTGTATCCAAAG 2220
2461 TATTTATATCAGAAATAGATGAGTCCGAAATTTTAAAGCTTATACCCGTTTATGAAATTAAGA 2520
2221 TATTTATATCAGAAATAGATGAGTCCGAAATTTTAAAGCTTATACCCGTTTATGAAATTAAGA 2280
2521 GGGTATATCAGAGATAGTCAAGACTTAGAATTTTATTTGATCGCGTACAATCAAAACAC 2580
2281 GGGTATATCAGAGATAGTCAAGACTTAGAATTTTATTTGATCGCGTACAATCAAAACAC 2340
2581 GAAATAGTAAATGTGCCAGGCAAGGTTCTTTATGCGCGCTTTCAGCCCAAGTCCAAATC 2640
2341 GAAATAGTAAATGTGCCAGGCAAGGTTCTTTATGCGCGCTTTCAGCCCAAGTCCAAATC 2400
2641 GGAAGTCTGAGAACCGAATCGATGCGGCGCACACCTTGAATGAAATCTCTGATCTAGAT 2700
2401 GGAAGTCTGAGAACCGAATCGATGCGGCGCACACCTTGAATGAAATCTCTGATCTAGAT 2460
2701 TGTTCTCTGAG 2711
2461 TGTTCTCTGAG 2471

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; Sequence 5, Application US/09972175
; Publication No. US20030101482A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; Mettus, Anne-Marie Light
; Gilmer, Amy Jelen
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
; LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/972,175
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
; APPLICATION DATA:
; FILING DATE: 09/337,635
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MECO:206
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3567
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-972-175-5

Query Match 89.6%; Score 2427.8; DB 11; Length 3567;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2444; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 241 ATGGAGGAATATCAAAATCAATGCATACCTTACAAATTTGTTAAAGTAATCTCTGAAGAA 300
DB 1 ATGGAGGAATATCAAAATCAATGCATACCTTACAAATTTGTTAAAGTAATCTCTGAAGAA 60
QY 301 GTACTTTGGATGAGGAGGATATCAATCAATCTGTAATTTACTCAATTTGATATTTCTGTCA 360
DB 61 GTACTTTGGATGAGGAGGATATCAATCAATCTGTAATTTACTCAATTTGATATTTCTGTCA 120
QY 361 CTGTTTCAGTTTCGTTATCTAATCTGTAATTTGTAACGAGGAGGATTTTAAAGTTGATTAATA 420
DB 121 CTGTTTCAGTTTCGTTATCTAATCTGTAATTTGTAACGAGGAGGATTTTAAAGTTGATTAATA 180
QY 421 GATTTTGTATGGGAATAGTTGGCCCTTCTCAATGGGATCTTCTAGTACAAATTTGAA 480
DB 181 GATTTTGTATGGGAATAGTTGGCCCTTCTCAATGGGATCTTCTAGTACAAATTTGAA 240
QY 481 CAATTAATTAATGAAGAATAGTCTGTAATTTGTAACGAGGAGGATTTTAAAGTTGATTAATA 540
DB 241 CAATTAATTAATGAAGAATAGTCTGTAATTTGTAACGAGGAGGATTTTAAAGTTGATTAATA 300
QY 541 GGATTAGGAACAAATTTCAATATATATGTGGAGCAATTTAAAGATGGGAAGATCTCT 600

301 GGATTAGGAACAAATTTCAATATATATGTGGAGCAATTTAAAGATGGGAAGATCTCT 360
QY 601 AATAATCCAGCAACACAGGACAGAGTAATTTGATCGCTTTTCGTATATCTTGATGGCTACTT 660
DB 361 AATAATCCAGCAACACAGGACAGAGTAATTTGATCGCTTTTCGTATATCTTGATGGCTACTT 420
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DB 421 GAAAGGGACATTTCTTCGTTTCGTAATTTCTGGATTTTGAAGTACCCCTTTATCCGTTTAT 480
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DB 541 TTGGGATTTGACAACGATAAATGTCAATGAAATCTATAATAGACTTCTGTAAATTTAGGCAATTTGAT 600
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DB 661 ACCTATCAAGATTTGGATAACATATATCGATTCGAGAGACTTAACATTTGACTGTATTA 720
QY 961 GATATCGCGCTTTCTTCCAAATAGCAATAGGAGATATCCAAATTCAGCCAGTTTGT 1020
DB 721 GATATCGCGCTTTCTTCCAAATAGCAATAGGAGATATCCAAATTCAGCCAGTTTGT 780
QY 1021 CAATTAACAGGAGATTTTACGACCCATTAATTTTAAATTTTAAATCCAGCTTACGCTCT 1080
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QY 1081 GTAGCTCAATTTACCTACTTTTAAAGCTTTTACGAGTATGAGTATTAAGAAATCTCATTTA 1140
DB 841 GTAGCTCAATTTACCTACTTTTAAAGCTTTTACGAGTATGAGTATTAAGAAATCTCATTTA 900
QY 1141 TTGATATATTTGAATAATCTTTACAAATCTTTTACGAGTATGAGTATGAGTATGAGTATGAGTAT 1200
DB 901 TTGATATATTTGAATAATCTTTACAAATCTTTTACGAGTATGAGTATGAGTATGAGTATGAGTAT 960
QY 1201 TATTGGGAGGACATCGAGTAAATATCTAGCTTTATAGGAGTGTGAACATAATCTCTCT 1260
DB 961 TATTGGGAGGACATCGAGTAAATATCTAGCTTTATAGGAGTGTGAACATAATCTCTCTCT 1020
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QY 1621 ACAATTTGATCCAGAGAGATTTAATCAATACCTTTTGTGAAAGATTTAGTATTTGGGG 1680

Db 1381 ACAATTGATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAAGATTAGAGTTTGGGGG 1440
Qy 1681 GGCACCTCTGTCATTAACAGACACGAGATTACAGGAGGGGATATCCTTCGAAGAAATACC 1740
Db 1441 GGCACCTCTGTCATTAACAGACACGAGATTACAGGAGGGGATATCCTTCGAAGAAATACC 1500
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Db 1561 TTAAGATTTGTCATCTACAGTCAATTAATTAATTCACCAATTAACCCAAAGATACCGT 1620
Qy 1861 TCCACAGGAGTGGGAGGCCAAGTTAGTGTAGATATGCTCTTCAGAAAACTATGGAATA 1920
Db 1621 TCCACAGGAGTGGGAGGCCAAGTTAGTGTAGATATGCTCTTCAGAAAACTATGGAATA 1680
Qy 1921 GGGGAGAACTTAACATCTAGAACATTTAGATATACCGATTTTAGTAATCCTTTTCAAT 1980
Db 1681 GGGGAGAACTTAACATCTAGAACATTTAGATATACCGATTTTAGTAATCCTTTTCAAT 1740
Qy 1981 AGAGCTAATCCAGATATAATTTGGATAAGTGAACCACTCTATTTGTCAGGTTCTATT 2040
Db 1741 AGAGCTAATCCAGATATAATTTGGATAAGTGAACCACTCTATTTGTCAGGTTCTATT 1800
Qy 2041 AGTAGCGTTGAACCTTTATATAGATAAAATTTGAAATTTATCTACAGATCAAAATTTGAA 2100
Db 1801 AGTAGCGTTGAACCTTTATATAGATAAAATTTGAAATTTATCTACAGATCAAAATTTGAA 1860
Qy 2101 GCAGATCTGATTTAGAAAGAGACAAAGAGCGGTGAATGCCCTGTTTACTTCTTCAAT 2160
Db 1861 GCAGATCTGATTTAGAAAGAGACAAAGAGCGGTGAATGCCCTGTTTACTTCTTCAAT 1920
Qy 2161 CAAATCGGTTAAAAACCGATGACGGATTATCATTTGATCAAGTATCCAAATTTAGTG 2220
Db 1921 CAAATCGGTTAAAAACCGATGACGGATTATCATTTGATCAAGTATCCAAATTTAGTG 1980
Qy 2221 GATTTGTTATCAGATGAATTTGTCGTGATGAAAGCGAGAAATTTGCCGAGAAATGCAAA 2280
Db 1981 GATTTGTTATCAGATGAATTTGTCGTGATGAAAGCGAGAAATTTGCCGAGAAATGCAAA 2040
Qy 2281 CATGCAAGGACTCAGTATGAGCGGAATTTACTTCAAGATCCAACTTCAGAGGATC 2340
Db 2041 CATGCAAGGACTCAGTATGAGCGGAATTTACTTCAAGATCCAACTTCAGAGGATC 2100
Qy 2341 AATAGACAACCGACCGTGGCTGGAGAGGAGTACAGATATTTACCAATCCAAAGGAGAT 2400
Db 2101 AATAGACAACCGACCGTGGCTGGAGAGGAGTACAGATATTTACCAATCCAAAGGAGAT 2160
Qy 2401 GAGCTATTCAAAGAGAAATACGTACACTACCGGTACCGTTGATGAGTGCTATCCAAG 2460
Db 2161 GAGCTATTCAAAGAGAAATACGTACACTACCGGTACCGTTGATGAGTGCTATCCAAG 2220
Qy 2461 TATTTATATCAGAAAAATAGATAGTCCGAAATTTAAAGCTTATACCCGTTATGAATTAAGA 2520
Db 2221 TATTTATATCAGAAAAATAGATAGTCCGAAATTTAAAGCTTATACCCGTTATGAATTAAGA 2280
Qy 2521 GGGTATATCGAAGATAGTCAAGACTTAGAAATCTATTGATCGCGTACAGATCCAAACAC 2580
Db 2281 GGGTATATCGAAGATAGTCAAGACTTAGAAATCTATTGATCGCGTACAGATCCAAACAC 2340
Qy 2581 GAAATAGTAAATGTCGAGGACCGGTTCTCTTATGCGCGCTTTCAGCCCCAAAGTCCAATC 2640
Db 2341 GAAATAGTAAATGTCGAGGACCGGTTCTCTTATGCGCGCTTTCAGCCCCAAAGTCCAATC 2400
Qy 2641 GGAAGTGTGGAGAACCGAATGATGCGGCCACACTTTGAATGGAATCCTGATCTAGAT 2700
Db 2401 GGAAGTGTGGAGAACCGAATGATGCGGCCACACTTTGAATGGAATCCTGATCTAGAT 2460
Qy 2701 TGTCTCTGCAG 2711
Db 2461 TGTCTCTGCAG 2471

RESULT 6

US-09-972-175-9
; Sequence 9, Application US/09972175
; Publication No. US20030101482A1
; GENERAL INFORMATION:

APPLICANT: Baum, James A.
; Gilmer, Amy Jelen
; Mettus, Anne-Marie Light

TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
; LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/972,175

FILING DATE: 05-Oct-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/337,635

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Kitchell, Barbara S.

REGISTRATION NUMBER: 33,928

REFERENCE/DOCKET NUMBER: MECO:206

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 3567 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 1..3567

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-972-175-9

Query Match 89.6%; Score 2427.8; DB 11; Length 3567;

Best Local Similarity 98.9%; Pred. No. 0;

Matches 2444; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 241 ATGGAGGAAAAATAATCAAAATCAATGCATACCTTCAATTTGTTAAGTAATCCTGAAGAA 300

Db 1 ATGGAGGAAAAATAATCAAAATCAATGCATACCTTCAATTTGTTAAGTAATCCTGAAGAA 60

Qy 301 GTACTTTTGGATGGAGAACGGATATCAACTGGTAATTAATCAATTTGATATTTCTCTGTCA 360

Db 61 GTACTTTTGGATGGAGAACGGATATCAACTGGTAATTAATCAATTTGATATTTCTCTGTCA 120

Qy 361 CTGTGTTCAAGTTTCTGGTATCTAACTTTGTACAGGGGGAGGATTTTAGTTGGATTAATA 420

Db 121 CTGTGTTCAAGTTTCTGGTATCTAACTTTGTACAGGGGGAGGATTTTAGTTGGATTAATA 180

Qy 421 GATTTTGTATGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTTAGTACAAATTGAA 480

Db 181 GATTTTGTATGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTTAGTACAAATTGAA 240

Qy 481 CAATTAATTAATGAAAGAAATAGCTGAATTTGCTAGGAATGCTGCTATTGCTAATTTAGAA 540

Db 540

Db	241	CAATTAATTAATGAAGAAATAGCTGAATTTGCTAGGAATGCTGCTATTTGCTAATTAAGAA	300
Qy	541	GGATTAGGAAACAAATTTCAATATATATGCGAAGCATTTAAAGAAATGGGAAGATCCT	600
Db	301	GGATTAGGAAACAAATTTCAATATATATGCGAAGCATTTAAAGAAATGGGAAGATCCT	360
Qy	601	AATTAATCCAGCAACCGAGCAGAGTAATGATTCGCTTTGCTATCTATCTATGATGGCTACTT	660
Db	361	AATTAATCCAGCAACCGAGCAGAGTAATGATTCGCTTTGCTATCTATCTATGATGGCTACTT	420
Qy	661	GAAGAGGACATTCCTTCGTTTCGAAATTTCTGGAATTTGAAGTTACCCCTTTTATCCGTTTAT	720
Db	421	GAAGAGGACATTCCTTCGTTTCGAAATTTCTGGAATTTGAAGTTACCCCTTTTATCCGTTTAT	480
Qy	721	GCTCAAGCGCCAAATCTGATCTAGCTATATTAAGAGATTTCTGTAATTTTTCGGAGAAAGA	780
Db	481	GCTCAAGCGCCAAATCTGATCTAGCTATATTAAGAGATTTCTGTAATTTTTCGGAGAAAGA	540
Qy	781	TTGGGATTTGAACAACGATAAATGTCATGAATACTATAATAGACTAATTAAGGCAATTCAT	840
Db	541	TTGGGATTTGAACAACGATAAATGTCATGAATACTATAATAGACTAATTAAGGCAATTCAT	600
Qy	841	GAATATGCTGATCAGCTGTGCAAAATACGTAATATCGGGGATTAATAATTTTACCGAAATCT	900
Db	601	GAATATGCTGATCAGCTGTGCAAAATACGTAATATCGGGGATTAATAATTTTACCGAAATCT	660
Qy	901	ACGTATCAAGATTTGGATAACATATAATCGATTAACGAGAGACTTTAACTGACTGTATTA	960
Db	661	ACGTATCAAGATTTGGATAACATATAATCGATTAACGAGAGACTTTAACTGACTGTATTA	720
Qy	961	GATATCCGCGCTTTCTTTCCAACTATGACATAGGAGATATCCAAATTCAGCCAGTTGGT	1020
Db	721	GATATCCGCGCTTTCTTTCCAACTATGACATAGGAGATATCCAAATTCAGCCAGTTGGT	780
Qy	1021	CAACTTAACAGGAGAGTTTATACGAGCCGATTAATTAATTTTATTCACAGTTTACAGTCT	1080
Db	781	CAACTTAACAGGAGAGTTTATACGAGCCGATTAATTAATTTTATTCACAGTTTACAGTCT	840
Qy	1081	GTAGTCAATTAACCTTCTTAAAGTTATGAGAGAGCGGCAATTTAGAAATCTCATTTA	1140
Db	841	GTAGTCAATTAACCTTCTTAAAGTTATGAGAGAGCGGCAATTTAGAAATCTCATTTA	900
Qy	1141	TTTGATATATTGAATTAATCTTAACTTTTACGATTTGTTAGTTGTTGAGCGCAATTTT	1200
Db	901	TTTGATATATTGAATTAATCTTAACTTTTACGATTTGTTAGTTGTTGAGCGCAATTTT	960
Qy	1201	TATTTGGGAGGACATCGAGTAATATCTAGCTTTATAGGAGTGGTAAACATACTCTCT	1260
Db	961	TATTTGGGAGGACATCGAGTAATATCTAGCTTTATAGGAGTGGTAAACATACTCTCT	1020
Qy	1261	ATATATGGAAGAGAGCGGAAACGAGAGCCTCCAAGATCCTTTATTTTAAATGAGCCGTA	1320
Db	1021	ATATATGGAAGAGAGCGGAAACGAGAGCCTCCAAGATCCTTTATTTTAAATGAGCCGTA	1080
Qy	1321	TTTATGAGCTTTATCAATTCCTTACTTTTACGATTTATACGCAACCTTGCAGCGCCACCAT	1380
Db	1081	TTTATGAGCTTTATCAATTCCTTACTTTTACGATTTATACGCAACCTTGCAGCGCCACCA	1140
Qy	1381	TTTAAATTTAGCTGCTGCAAGGATGAGATTTTCTACACCTTACAAATAGCTTTACGTAT	1440
Db	1141	TTTAAATTTAGCTGCTGCAAGGATGAGATTTTCTACACCTTACAAATAGCTTTACGTAT	1200
Qy	1441	CGAGAGAGGTACGGTTGATTTCTTAACTGAATTAACCGCTGAGGATATAGTGTCCA	1500
Db	1201	CGAGAGAGGTACGGTTGATTTCTTAACTGAATTAACCGCTGAGGATATAGTGTCCA	1260
Qy	1501	CCTCGCGAAGGATATAGTCATCGTTTATATGTCATGCAACTTTTGTTCGAAGATCTGMAA	1560
Db	1261	CCTCGCGAAGGATATAGTCATCGTTTATATGTCATGCAACTTTTGTTCGAAGATCTGMAA	1320
Qy	1561	CCTTTTTTAAACATCGTGTAGTATTTTCTTGGACGCACTCGTAGTGGCACTTTTACAAAT	1620
Db	1321	CCTTTTTTAAACATCGTGTAGTATTTTCTTGGACGCACTCGTAGTGGCACTTTTACAAAT	1380
Qy	1621	ACAATTTGATCCAGAGAGAAATTAATCAAAATACCTTTTAGTGAAAGGATTTAGAGTTGGGG	1680
Db	1381	ACAATTTGATCCAGAGAGAAATTAATCAAAATACCTTTTAGTGAAAGGATTTAGAGTTGGGG	1440
Qy	1681	GGCACTCTGCTCATTTACAGGACACAGGATTTACAGGAGGGGATATCTTTCGAAAGAAATACC	1740
Db	1441	GGCACTCTGCTCATTTACAGGACACAGGATTTACAGGAGGGGATATCTTTCGAAAGAAATACC	1500
Qy	1741	TTTGTGATTTTGTATCTCTACAGTCAATATTAATTCACCAATTTACCCAAAGATACCGT	1800
Db	1501	TTTGTGATTTTGTATCTCTACAGTCAATATTAATTCACCAATTTACCCAAAGATACCGT	1560
Qy	1801	TTTAGATTTTGTATCGCTTCAGTAGGATGCGAGTATAGTATTAATTAACAGGAGCGCA	1860
Db	1561	TTTAGATTTTGTATCGCTTCAGTAGGATGCGAGTATAGTATTAATTAACAGGAGCGCA	1620
Qy	1861	TCCACAGAGTGGGAGGCGCAAGTTAGTGTAGATATGCTCTTCAGAAACTATGGAATA	1920
Db	1621	TCCACAGAGTGGGAGGCGCAAGTTAGTGTAGATATGCTCTTCAGAAACTATGGAATA	1680
Qy	1921	GGGAGAACTTAACATCTTAGAAACATTTAGATATACCGATTTTGTATCTTTTTCATTT	1980
Db	1681	GGGAGAACTTAACATCTTAGAAACATTTAGATATACCGATTTTGTATCTTTTTCATTT	1740
Qy	1981	AGACTTAATCCAGATATAATTTGGGATAGTGAACAACTCTATTTTGTGCGAGTTCTATT	2040
Db	1741	AGACTTAATCCAGATATAATTTGGGATAGTGAACAACTCTATTTTGTGCGAGTTCTATT	1800
Qy	2041	AGTAGCGTTGAACTTTATATAGATAAAATTTGAAATTTTCTAGCAGATGCAACATTTGAA	2100
Db	1801	AGTAGCGTTGAACTTTATATAGATAAAATTTGAAATTTTCTAGCAGATGCAACATTTGAA	1860
Qy	2101	CGAGAACTCTGATTTAGAAAGAGCACAAAGGCGGTGAATGCGCTTTTACTTCTTCCAAT	2160
Db	1861	CGAGAACTCTGATTTAGAAAGAGCACAAAGGCGGTGAATGCGCTTTTACTTCTTCCAAT	1920
Qy	2161	CAAAATCGGTTTAAAAACCGATGTCACCGATTTATCATTTGATCAAGTATCCAATTTAGTG	2220
Db	1921	CAAAATCGGTTTAAAAACCGATGTCACCGATTTATCATTTGATCAAGTATCCAATTTAGTG	1980
Qy	2221	GATTTGTTTATCAGATGAATTTTGTCTCGATGAAAGCGGAAATTTGTCGAGAAAGTCAAA	2280
Db	1981	GATTTGTTTATCAGATGAATTTTGTCTCGATGAAAGCGGAAATTTGTCGAGAAAGTCAAA	2040
Qy	2281	CATCGGAAGCGACTCAGTGATGAGCGGAATTTACTTCAAGATCCAAACTTTCAGAGGATC	2340
Db	2041	CATCGGAAGCGACTCAGTGATGAGCGGAATTTACTTCAAGATCCAAACTTTCAGAGGATC	2100
Qy	2341	AATAGACAAACAGACCCGCTGCGAGAGGAGTACAGATTTTACATCCAGAGGAGAT	2400
Db	2101	AATAGACAAACAGACCCGCTGCGAGAGGAGTACAGATTTTACATCCAGAGGAGAT	2160
Qy	2401	GACGTTATTCAAAGAGAAATTCGTCACTACCGGGTACCGTTGATGAGTGTATCCAACG	2460
Db	2161	GACGTTATTCAAAGAGAAATTCGTCACTACCGGGTACCGTTGATGAGTGTATCCAACG	2220
Qy	2461	TATTTATATCAGAAAAATAGATGAGTTCGAAATTTAAAGCTTATACCCGTTATGAATTAAGA	2520
Db	2221	TATTTATATCAGAAAAATAGATGAGTTCGAAATTTAAAGCTTATACCCGTTATGAATTAAGA	2280
Qy	2521	GGGTATATCAGAAATAGTCAAGACTTGAATACTATTTGATCGCGTACAATGCAAAACAC	2580
Db	2281	GGGTATATCAGAAATAGTCAAGACTTGAATACTATTTGATCGCGTACAATGCAAAACAC	2340
Qy	2581	GAATAGTAAATGTCAGCGACCGGTTTCTTATGCGCTTTTACGCCCTTACGAGGATC	2640
Db	2341	GAATAGTAAATGTCAGCGACCGGTTTCTTATGCGCTTTTACGCCCTTACGAGGATC	2400
Qy	2641	GGAAAGTGTGGAAACCGAATCGATGCGCCACACTTGAATGGAATCTCTGATCTAGAT	2700
Db	2401	GGAAAGTGTGTGGAAACCGAATCGATGCGCCACACTTGAATGGAATCTCTGATCTAGAT	2460

Qy 2701 TGTTCTGCAG 2711
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Db 2461 TGTTCTGCAG 2471

RESULT 7

US-09-972-175-7
; Sequence 7, Application US/03972175
; Publication No. US20030101482A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.

**TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS**

NUMBER OF SEQUENCES: 76

NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:

ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

FILE. 77210
COMPUTER READABLE FORM:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0 Version #1.30

SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/
FILING DATE: 05-05-2001

FILING DATE: 05-Oct-2011

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Kitchell, Barbara S.

REGISTRATION NUMBER: 33,912

REFERENCE/DOCKET NUMBER

TELECOMMUNICATION INFORMATION

TELEPHONE: 512/418-3000

TELEPHONE: 512/474-3000
TELEFAX: 512/474-7577

INFORMATION: FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 3567 base pairs

TYPE: nucleic acid

**LIFE: NUCLEIC ACID
STRANDEDNESS: single**

STRANDEDNESS: Single
TOPOLOGY: Linear

TOPOLOGY: Linear
FEATURE:

FEATURE:	NAME/KEY:	CDS
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100	100	100

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Query Match      89.5%; Score 2426.2; DB 11; Length 3567;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2443; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
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241	ATGAGAGAAATTAATCAAATCAATGATACCTTTACAATTTGTTTAAAGTAATCTTGAAGAA	300
Qy		
Db		
1	ATGAGAGAAATTAATCAAATCAATGATACCTTTACAATTTGTTTAAAGTAATCTTGAAGAA	60
Qy		
301	GTACTTTTGGATGGAGAACGGATATCAACTGGTAAATTACTCAAATTGATATTTCTCTGTCA	360
Qy		
Db		
61	GTACTTTTGGATGGAGAACGGATATCAACTGGTAAATTACTCAAATTGATATTTCTCTGTCA	120
Qy		
361	CTTGTTTCAGTTTCTGGTATCTAACTTTGTGTACCGGGGAGGATTTTGTAGTTGGAATTAATA	420
Qy		
Db		
121	CTTGTTTCAGTTTCTGGTATCTAACTTTGTGTACCGGGGAGGATTTTGTAGTTGGAATTAATA	180
Qy		
421	GATTTTGTATGGGGAAATAGTTGGCCCTTCTCAATGGGATGATTTCTAGTACAAATTTGAA	480
Qy		
Db		
181	GATTTTGTATGGGGAAATAGTTGGCCCTTCTCAATGGGATGATTTCTAGTACAAATTTGAA	240
Qy		

QY 1561 CTTTCTTTTAACTGGTGTAGTATTTCTTGGAGCATCGTAGTCACTCTTACAAAT 1620
Db 1321 CTTTCTTTTAACTGGTGTAGTATTTCTTGGAGCATCGTAGTCACTCTTACAAAT 1380
QY 1621 ACAATTGATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGGATTTAGATTGGGGG 1680
Db 1381 ACAATTGATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGGATTTAGATTGGGGG 1440
QY 1681 GGCACCTCTGTCTATTACAGGACAGGATTTACAGAGGGGATATCTTCCGAAGAAATACC 1740
Db 1441 GGCACCTCTGTCTATTACAGGACAGGATTTACAGAGGGGATATCTTCCGAAGAAATACC 1500
QY 1741 TTTGGTGAATTTGTATCTCTACAGTCAATATTAATCACCAGTATACCCAAAGATACCGT 1800
Db 1501 TTTGGTGAATTTGTATCTCTACAGTCAATATTAATCACCAGTATACCCAAAGATACCGT 1560
QY 1801 TTAAGATTTTCGTAGCTTCCAGTACGAGTGCAGAGTATAGTATTAACAGAGCGGCA 1860
Db 1561 TTAAGATTTTCGTAGCTTCCAGTACGAGTGCAGAGTATAGTATTAACAGAGCGGCA 1620
QY 1861 TCCACAGGATGGAGCGCAAGTTAGTGTAGATATGCTCTTCGAAACTATGGAATA 1920
Db 1621 TCCACAGGATGGAGCGCAAGTTAGTGTAGATATGCTCTTCGAAACTATGGAATA 1680
QY 1921 GGGGAGAACTTAACTAGAGAACTTTAGATATACCGATTTTAGTATCTTTTCAATTT 1980
Db 1681 GGGGAGAACTTAACTAGAGAACTTTAGATATACCGATTTTAGTATCTTTTCAATTT 1740
QY 1981 AGAGCTAATCCAGATATTAATTTGGGATAAGTGAACAACTCTATTGTCAGGTTCTATT 2040
Db 1741 AGAGCTAATCCAGATATTAATTTGGGATAAGTGAACAACTCTATTGTCAGGTTCTATT 1800
QY 2041 AGTAGCGTTGAACTTTATATAGATAAAATTTGAAATTTTCTAGCAGATCAACATTTGAA 2100
Db 1801 AGTAGCGTTGAACTTTATATAGATAAAATTTGAAATTTTCTAGCAGATCAACATTTGAA 1860
QY 2101 GCAGATCTGATTTAGAAAGAGACAAAAGGCGGTGAATGCCCTGTTTACTTCTTCCAAT 2160
Db 1861 GCAGATCTGATTTAGAAAGAGACAAAAGGCGGTGAATGCCCTGTTTACTTCTTCCAAT 1920
QY 2161 CAATCGGTTTAAACCGATGTCGAGGATTTATCATATGATCAAGTATCAATTTAGTG 2220
Db 1921 CAATCGGTTTAAACCGATGTCGAGGATTTATCATATGATCAAGTATCAATTTAGTG 1980
QY 2221 GATGTTTATCAGATGAATTTCTGCTGGATGAAGAGAGGATTTCCGAGAACTCAA 2280
Db 1981 GATGTTTATCAGATGAATTTCTGCTGGATGAAGAGAGGATTTCCGAGAACTCAA 2040
QY 2281 CATGCGAAGGACTCAGTGTAGAGCGGAATTTACTTCAAGATCCAACTTCAGAGGATC 2340
Db 2041 CATGCGAAGGACTCAGTGTAGAGCGGAATTTACTTCAAGATCCAACTTCAGAGGATC 2100
QY 2341 AATAGACACACGACCGTGGCTGGAGAGGAGTACAGATATTACCATCCAAGGAGAGAT 2400
Db 2101 AATAGACACACGACCGTGGCTGGAGAGGAGTACAGATATTACCATCCAAGGAGAGAT 2160
QY 2401 GAGGTATCCAAAGAGAAATACGTCACACTACCGGTCGCTGATGAGTGTATCCAAAG 2460
Db 2161 GAGGTATCCAAAGAGAAATACGTCACACTACCGGTCGCTGATGAGTGTATCCAAAG 2220
QY 2461 TATTTATATCAGAAATAGATGAGTCGAAATTAAGGCTTATACCCGTTATGAAATTAAGA 2520
Db 2221 TATTTATATCAGAAATAGATGAGTCGAAATTAAGGCTTATACCCGTTATGAAATTAAGA 2280
QY 2521 GGGTATATCGAAGATAGTCAAGACTTAGAATCTATTTGTCGGTACATCAAAACAC 2580
Db 2281 GGGTATATCGAAGATAGTCAAGACTTAGAATCTATTTGTCGGTACATCAAAACAC 2340
QY 2581 GAATATGAATATGTCGAGGAGGCTTCTTATGAGGCTTTTCAGGCCAAAGTCCAAATC 2640
Db 2341 GAATATGAATATGTCGAGGAGGCTTCTTATGAGGCTTTTCAGGCCAAAGTCCAAATC 2400
QY 2641 GGAAAGTGTGGAGAAACCGAATCGATGCGCGCCACACCTTGAATGGAAATCTGTATAGT 2700

Db 2401 GGAAAGTGTGGAGAAACCGAATCGATGCGCGCCACACCTTGAATGGAAATCTGTATAGT 2460
QY 2701 TGTTCCTGCAG 2711
Db 2461 TGTTCCTGCAG 2471
RESULT 8
US-09-972-175-58
; Sequence 58, Application US/09972175
; Publication No. US20030101482A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; Mettus, Anne-Marie Light
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
; LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,175
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/337,635
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MECO:206
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-2577
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3567 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3567
; SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-972-175-58
Query Match 89.3%; Score 2419.8; DB 11; Length 3567;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2439; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 241 ATGAGAGAAAATAATCAAAATCAATGCATACCTTACAAATGTTTAAGTAATCTCTGAAGAA 300
Db 1 ATGAGAGAAAATAATCAAAATCAATGCATACCTTACAAATGTTTAAGTAATCTCTGAAGAA 60
QY 301 GTACTTTTGGATGGAGACGGATATCAACTGGTAATTAATCTCAATTTGATTTCTCTGTCA 360
Db 61 GTACTTTTGGATGGAGACGGATATCAACTGGTAATTAATCTCAATTTGATTTCTCTGTCA 120
QY 361 CTTCTTCAGTTCTGTATCAACTTTGTACACGGGGAGGATTTTGTAGTTGGATTAATA 420
Db 121 CTTCTTCAGTTCTGTATCAACTTTGTACACGGGGAGGATTTTGTAGTTGGATTAATA 180

421 GATTTTGTATGGGAATAGTTGGCCCTCTCAATGGATGCAATTTCTAGTACAAATGAA 480
181 GATTTTGTATGGGAATAGTTGGCCCTCTCAATGGATGCAATTTCTAGTACAAATGAA 240
481 CAATTAATTAATGAAGAATAGTGAATTTGCTAGGAATGCTGCTATTTGCTAATTTAGAA 540
241 CAATTAATTAATGAAGAATAGTGAATTTGCTAGGAATGCTGCTATTTGCTAATTTAGAA 300
541 GGATTAAGGAACAAATTTCAATATATATATGTGGGAAGCAATTTAAAGAAATGGGAAGATCCT 600
301 GGATTAAGGAACAAATTTCAATATATATATGTGGGAAGCAATTTAAAGAAATGGGAAGATCCT 360
601 AATAATCCAGCAACCAAGGACCAAGTAATTTGATCGCTTTGCTATGATGCTGCTACTT 560
361 AATAATCCAGCAACCAAGGACCAAGTAATTTGATCGCTTTGCTATGATGCTGCTACTT 420
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421 GAAAGGCAATTCCTTTCGTTTCGAAATTTCTGGAAATTTGAAAGTACCCCTTTTATCCGTTTAT 480
721 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAAATTTTGGAGAAAGA 780
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781 TTGGGATTCACAACGATAATGTCAATGAATACTAATAGACTAATTAAGGCAATTTGAT 840
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841 GAATATGCTGATCAGTGTGCAATACGTATATTCGGGGATTTAAATTTTACCGAATCT 900
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781 CAACTAAAGGAAGTGTATACGGACCAATTAATTTTAAATCCACAGTTACAGTCT 840
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901 TTGTATATATGAAATCTTACAAATCTTTACGAATGTTGTTAGTTGGACGCAATTTT 960
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961 TATTTGGGAGGACATCGAGTAATATCTAGCCTTATAGGAGTGGTAAACATACATCTCT 1020
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1321 TTTAGACATTTATCAATTCCTACTTTTAAATCGATTTATACAGAACCTTTGCCAGGCCACCA 1380
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1261 CCTCGGAAGGATATAGTCATCGTTTATAGTCACCAATTTTGTTCAAAGATCTGGAACA 1320
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1861 GCGAATCTGATTTAGAAAGGACCAAAAGCGGTGAATGCCCTGTCTTCTTCCCAAT 1920
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2161 GACGTATTTCAAAGAGAAATTTAGTCACTACCGGGTACCGTTGATGAGTGTATCCAAG 2220
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Db	2341	GAATAGTAAATGTCCAGGCACGGGTCTTCTATGGCGCGCTTCAGGCCAAAGTCTCAATC	2400
Qy	2641	GGAAAGTGTGGAGAACCGAATCGATGCGCGGCACACCTTGAATGAATCTTGATCTAGAT	2700
Db	2401	GGAAAGTGTGGAGAACCGAATCGATGCGCGGCACACCTTGAATGAATCTTGATCTAGAT	2460
Qy	2701	TGTTCTCTGCAG	2711
Db	2461	TGTTCTCTGCAG	2471

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1  RESULT 9
2  US-09-972-175-60
3  ; Sequence 60, Application US/09972175
4  ; Publication No. US20030101482A1
5  ; GENERAL INFORMATION:
6  ;
7  ; APPLICANT: Baum, James A.
8  ; Glimmer, Amy Helen
9  ; Metcub, Anne Marie Light
10 ;
11 ; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
12 ; TRANSEPTIN-ACTIVE-DELTAB-EPITOXINS

```

NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/972,175
FILING DATE: 05-OCT-2001

CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/337,635
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.

NAME: ALACRACY, EUGENE
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206

TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000

TELEPHONE: 512/474-7577
TELEFAX: 512/474-7577
INFORMATION FOR SEO ID NO: 60:

SEQUENCE CHARACTERISTICS:
LENGTH. 3567 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

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; SINGLES: single  
; TOPOLOGY: linear  
FEATURE:
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FEATURE:	NAME/KEY:	CDS
	LOCATION:	1 3567

LOCATION:	SEQUENCE DESCRIPTION:	SEQ ID NO:	60:
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US-09-972-175-60
.
Current Match 89 2%. Score 2418.2

Query Match	98.7%
Best Local Similarity	98.7%
Best Global Similarity	98.7%
Conservative	98.7%
Aggressive	98.7%
Pred. No. 0;	0
Mismatch	0

Matches 2438; conservative 0; progressive 0

241 A TGGAGGATTAACCATTCCTCCTCC
|||||
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DB I ATGGAGGAGAAATATACTTTCCTTTCCCTTT

301
31
32

61 GIACIIIGGAGGAGTCCGHHIIGIIGI

[illegible]

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181	DB	GATTTTGTATGGGGAATAGTTGGCCCTTCTCAATGGGATGCATTTCTAGTACAAATGGAA	240
481	QY	CAATTAATTAATGAAGAAATAGCTGAATTTGCTAGGAATGCTGTAATTCCTAATTTAGAA	540
241	DB	CAATTAATTAATGAAGAAATAGCTGAATTTGCTAGGAATGCTGTAATTCCTAATTTAGAA	300
541	QY	GGTTTGGGAACAAATTTCAATATATGTCGAAGCAATTTAAAGAAATCGGAAGAGATCCT	600
301	DB	GGTTTGGGAACAAATTTCAATATATGTCGAAGCAATTTAAAGAAATCGGAAGAGATCCT	360
601	QY	AATATATCCGACACGACGACGAGTAAATGATCGCTTTCGTATACATTGATGGGGTACTT	660
361	DB	AATATATCCGACACGACGACGAGTAAATGATCGCTTTCGTATACATTGATGGGGTACTT	420
661	QY	GAAGGGGACATTCCTTCGTTTCGAAATTCCTGGAATTTGAAGTACCCCTTTTTATCCGGTTAT	720
421	DB	GAAGGGGACATTCCTTCGTTTCGAAATTCCTGGAATTTGAAGTACCCCTTTTTATCCGGTTAT	480
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541	DB	TTGGGATTTGACAAGCATAAATGTCAAATGCAAACTAATATAGACTAAATTTAGSCATAATGAT	600
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601	DB	GAATATGCTGTATCTACTGTGCAAAATAGTATATCCGGGATTAATTAATTTACCGGCTAGC	660
901	QY	ACGTATCAAGATTTGGATAACAATATAATCGATTACGGHAGACCTTAACATGACTGTATTA	960
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721	DB	GATATCCGCGCTTTCTTTCCAAACTATGACAATAGGAGATATCCAAATTTACGCCAGTTGGT	780
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781	DB	CAACTAACAGGGAAGTTTATACGGACCCATTAATTTAATTCACAGTTACAGTCT	840
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841	DB	GTAGTCCAAATTAACCTACTTTTAAACGGTTATGGHAGACGCGCAATTAGAAATCTCATTTA	900
1141	QY	TTTGATATATTGAAATAACTCTTCAAACTTTTACGGATTTGTTTGTGTGGACGCAATTTT	1200
901	DB	TTTGATATATTGAAATAACTCTTCAAACTTTTACGGATTTGTTTGTGTGGACGCAATTTT	960
1201	QY	TATTTGGGAGGACATCGAGTAAATATCTAGCCCTTATAGAGGTGGTAAACATAACATCTCCT	1260
961	DB	TATTTGGGAGGACATCGAGTAAATATCTAGCCCTTATAGAGGTGGTAAACATAACATCTCCT	1020
1261	QY	ATATATGGAAGAGCGGCAACGAGGACCTTCAAGATCTCTTTTATTTTAAATGGACCGGTA	1320
1021	DB	ATATATGGAAGAGCGGCAACGAGGACCTTCAAGATCTCTTTTATTTTAAATGGACCGGTA	1080
1321	QY	TTTGGAGCTTTTCAATTCCTACTTTTACGATTAATATACAGCAACCTTGGCAGCGGCCAAT	1380
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1381	QY	TTTTAATTTTACGTGGTGTCAAGAGTAGAATTTTCTACACCTACAAATAGCTTTTACGTAT	1440
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1441	QY	CGAGGAGAGGTACGGTTCATTTCTTTAACTGMAATACGCCCTGAGGATTAATAGTGTGCCA	1500

Db 1201 CGAGGAGAGGTACGGTTCATCTTTAACTGAATTAACCCCTGAGGATTAATAGTGGCA 1260
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Db 1261 CCTCGGAAGGATATAGTTCATCGTTTATGTCATGCAACTTTTGTTCAAAGATCTGGAA 1320
Qy 1561 CCTTTTAACTCGGTGTAGTATTTCTTGGACGATCGTAGTGCAACTCTCTTCAAAAT 1620
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Db 1441 GGCACCTCTGTCAATACAGGACAGGATTAACAGGAGGGATATCCTTCGAAGAAATACC 1500
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Db 1621 TCCACAGAGTGGGAGCCCAAGTTAGTGTAAATATGCTCTTCAGAAACTATGGAATA 1680
Qy 1921 GGGGAGAACTTAACATCTAGAACATTTAGATATACCGATTTAGTAATCTCTTTTCATTT 1980
Db 1681 GGGGAGAACTTAACATCTAGAACATTTAGATATACCGATTTAGTAATCTCTTTTCATTT 1740
Qy 1981 AGAGCTAATCCAGATATTAATGCGATAAGTGAACACCTCTATTTGGTGACGTTCTATT 2040
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Db 1801 AGTAGCGTTGAACCTTTATATAGATAAAATTTGAAATTTATCTAGCAGATCAACATTTGAA 1860
Qy 2101 CGAGATCTGATTTAGAAAGAGACAAAGGCGGTGAATGCGCTGTCTTACTTCTTCCAAAT 2160
Db 1861 CGAGATCTGATTTAGAAAGAGACAAAGGCGGTGAATGCGCTGTCTTACTTCTTCCAAAT 1920
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Qy 2221 GATTTGTTATCAGATGAATTTTGTCTGATGAAAGCGAGAAATGTCGAGAAAGTCAAA 2280
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Qy 2581 GAAATAGTAAATGTCCAGGACCGGTTCTTTATGCGCGCTTTTTCAGCCCAAGTCCAATC 2640
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Qy 2641 GGAAGTGTGGAGAACCGAATCGATGCGGCGCACACCTTGAATGAATCTCTGATCTAGAT 2700
Db 2401 GGAAGTGTGGAGAACCGAATCGATGCGGCGCACACCTTGAATGAATCTCTGATCTAGAT 2460
Qy 2701 TGTTCCTGCAG 2711
Db 2461 TGTTCCTGCAG 2471

RESULT 10

US-09-826-660-20
; Sequence 20, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 3489
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic B.t. toxin gene
US-09-826-660-20

Query Match 63.9%; Score 1733.2; DB 9; Length 3489;
Best Local Similarity 82.4%; Pred. No. 0;
Matches 1987; Conservative 0; Mismatches 423; Indels 0; Gaps 0;

Qy 241 ATGGAGGAAATTAATCAAAATCAATGATACCTTCAATTTGTTAAGTAATCTCGAAGNA 300
Db 1 ATGGAGGAGAAACAATCAGAAATCAGTGCATACCTTCAAACTGCTTGAGCAATCTGGAAGAG 60
Qy 301 GTACTTTTGGATGGAGAACGGATATCAACTGTGAATTAATCAATTTGATTTCTCTGTCA 360
Db 61 GTACTTTTGGATGGAGAACGGATATCAACTGTGAATTAATCAATTTGATTTCTCTGTCA 120
Qy 361 CTGTGTCAGTTTCTGATCTAACTTTGTACAGGGGAGGATTTTGTGATTAATA 420
Db 121 CTGTGTCAGTTTCTGATCTAACTTTGTACAGGGGAGGATTTTGTGATTAATA 180
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Db 181 GACTTTGTGGGGCAATTTGTTGGCCCATCTCAATGGGATGCTTCTTGTGACAGATTGAA 240
Qy 481 CAAATTAATTAAGAAAGATAGCTGAATTTGCTAGGAATGCTGCTATTTAGTAATTTAGAA 540
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Db 301 GGATAGGAACAATTTCAATATATATGTTGAAGCATTTAAAGAAATGGGAAGATCCT 360
Qy 601 AATTAATCAGCAACCCAGGACAGAGTAATGATCGCTTTTGTATATCTTGTATGATGGGCTACTT 660
Db 361 AACATCCAGCAACCCGTAACGAGATCATTTGATCGCTTTTGTATATCTTGTATGATGGGCTACTT 420


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; FILE REFERENCE: MECO:210--2
; CURRENT APPLICATION NUMBER: US/09/873,873
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 09/253,341
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 08/922,505
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
US-09-873-873-29

Query Match      55.3%; Score 1498.2; DB 9; Length 3579;
Best Local Similarity 77.5%; Pred. No. 1.1e-310;
Matches 1924; Conservative 0; Mismatches 508; Indels 51; Gaps 7;

QY 259 AATCAATGCATACCTTACAAATGTTTAAAGTAACTCCTGAAGAGTACTTTTGGATGAGAA 318
DB 22 AATGAATGCATTCCTTATTAATGTTTAAAGTAACTCCTGAAGAGTAAAGTATTTAGGTGGAGAA 81
QY 319 CGGATATCAACTGGTAAATTAATCAATTTGATATTTCTGTCACTTGTTCAGTTCTCTGGTA 378
DB 82 AGAATAGAACTGGTTACACCCCAATCGATATTTCTCTGTCTGCTAAGCAATTTCTTTTG 141
QY 379 TCTAACTTTGTACAGGGGAGATTTTGTAGTTGAATTAATAGATTTTGTATGGGGAATA 438
DB 142 AGTGAATTTGTTCCCGGTGCTGATTTGTGTAGGACTAGTTGATATAATATATGGGAAAT 201
QY 439 GTTGGCCCTCTCAATGGGATGCAATTTCTAGTACAAATTTGAACAATTAATTAATGAAGA 498
DB 202 TTGTGGTCCCTCAATGGGAGCGATTTCTGTGACAAATTTGAACAGTAAATTAACCAAGA 261
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DB 262 ATAGAAGATTTGCTAGGAACCAAGCCATTTCTAGATTAAGAGGACTAAGCAATCTTTAT 321
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DB 442 TTTGCAATTTCAAAATATCAAGTTCTCTTTTATCAAGTATATGTTCAAGCTGCAAAATTTA 501
QY 739 CATCTAGCTATTAAGAGATCTGTAAATTTTGGGAAGAGATTTGGGATTTGACACGATA 798
DB 502 CATTTATCAGTTTGGAGATGTTTCAGTGTTTGGACAAAGGTGGGATTTGATGCGCG 561
QY 799 AATGTCATGAACAACTATTAATAGACTAATTAGGCATATTTGATGAATATGCTGATCACTGT 858
DB 562 ACTATCAATAGTCGTTATTAATGATTTAACTAGGCTTTAATGGCAACTATACAGATTAATGCT 621
QY 859 GCAAAATACGTATAATCGGGGATTTAAATAATTTACCGAAATCTACGTATCAAGATTTGGATA 918
DB 622 GTACGCTGTATCAATACGGGATTTAGAACGTGTATGGGGACCGGATTTAGAGATTTGGGTA 681
QY 919 ACATATAATCGATTTACGGAGAGACTTAAACATTTGACTGTATTAGATATCCCGCTTTCTTT 978
DB 682 AGGTATAATCAATTTAGAGAGAAATTAACACTAACTGTATTAGATATCGTTGCTCTGTTTC 741
QY 979 CCAAACTATGACAAATAGGAGATATCCAAATTTAGCCAGTGTGGTCAACTAACAGGGAAGTT 1038
DB 1038 CCAAACTATGACAAATAGGAGATATCCAAATTTAGCCAGTGTGGTCAACTAACAGGGAAGTT 1038
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DB 742 CCGAATATGATAGTAGAAGATATCCAAATTCGAAACAGTTTCCAAATTAACAAGAGAAAT 801
QY 1039 TATACGGACCCATTAATTAATTTTAAATCCACAGTTTACAGTCTGTAGCTCAATTTACCTACT 1098
DB 802 TATACAAACCCAGTATTAGA-----AAATTTGATGGTAGTTTTCAGGC 846
QY 1099 TTTAAGCTTATCGAGAGCAGCGCAATTAGAAATCTCTCATTTATTTTATTTGATATTTGAATAAT 1158
DB 847 TCGGCTCAGGGCATAGAAAGAGTATTAGGAGTCCACATTTGATGATATCTTAAACAGT 906
QY 1159 CTTTCAATCTTTTACCGATTTGTTAGTGTGGACGCAATTTTATTTGGGAGGACATCGA 1218
DB 907 ATAACCATCTATACGGATGCTCATAGG-----GTTATATTTATTTGGTCAGGCAATCAA 960
QY 1219 GTAATATCTAGCCTTATAGG-----AGGTGGTAAACATAACATCTCTATATATGGAAGA 1272
DB 961 ATAATGGCTTCTCTCTAGGGTTTTCGGGGCCAGAAATTCACATTTCCGCTATATGGAAT 1020
QY 1273 GAGGCAACCCAGAGGCTCCAAGATCTCTTTTAA-----TGGACCGGTATTTAGGACT 1329
DB 1021 ATGGGAAATGCACTCCACAAACAGTATTTGTTGCTCAACTAGGTCAAGGCGGTATAGA 1080
QY 1330 TTATCAATCTCTACTTACGATTTATACAGCAACCTTGCAGCGGCCACCATTTTATTTA 1389
DB 1081 ACAATATCTGCTCACATTTATATAGAGACCTTTTAAATATAGGATAAATAATCAACAATA 1140
QY 1390 CGTGTGGTGAAGAGTAGTAATTTTCT-----ACACCTCAAAATAGCTTTTACG----- 1437
DB 1141 TCTGTTCTTGACGGGACAGAAATTTGCTTATGGAACTCTCTCAATTTGCAATCCGCTGTA 1200
QY 1438 TATCAGGAAGAGGTACGTTGATTTCTTTTAACTGAATTAACCGCTGAGGATTAATAGTGTG 1497
DB 1201 TACAGAAAAGCGGACGAGTATCGCTGGATGAATACCGCCACAGAAATAACAACGTG 1260
QY 1498 CCACCTCGGAGGATATAGTCACTCGTTTATGCTATGCACTGCAACTTTTGTTC-----AA 1548
DB 1261 CCACCTAGGCAAGGATTTAGTCACTCGATTAAGCCATTTTCAATGTTTCTGTTCAAGCTTT 1320
QY 1549 AGATCTGGAACACCTTTTAACTAAGTGTAGTATTTCTTGGACGATCGTACTGCA 1608
DB 1321 AGTAATAGTAGTAAAGTATAATAGAGCTCTATGTTCTCTTGGATACATCGTAGTGCA 1380
QY 1609 ACTCTTACAAATCAATTTGATCCAGAGAGAAATTAATCAAAATACCTTTTGTGAAAGGATTT 1668
DB 1381 ACTCTTACAAATCAATTTGATCCAGAGAGAAATTAATCAAAATACCTTTTGTGAAAGGATTT 1440
QY 1669 AGAGTTTGGGGGGGACCTCTCTGATACAGACAGAGATTTACAGGAGGAGATATCCTT 1728
DB 1441 AGAGTTTGGGGGGGACCTCTCTGATACAGACAGAGATTTACAGGAGGAGATATCCTT 1500
QY 1729 CGAAGAAATACCTTTTGGTGTATTTGCTATCTCTACAAGTCAATTAATTAATTCACCAATTACC 1788
DB 1501 CGAAGAAATACCTTTTGGTGTATTTGATCTCTACAAGTCAATTAATTAATTCACCAATTACC 1560
QY 1789 CAAAGATACCGTTTAAAGATTTCTGTTACGCTTCCAGTAGGAGTGCAGCAGTTATAGTATTA 1848
DB 1561 CAAAGATACCGTTTAAAGATTTCTGTTACGCTTCCAGTAGGAGTGCAGCAGTTATAGTATTA 1620
QY 1849 ACAGAGCGGCATCCACAGGAGTGGAGGCGCAAGTTAGTGTAGATATGCTCTCTCAGAAA 1908
DB 1621 ACAGAGCGGCATCCACAGGAGTGGAGGCGCAAGTTAGTGTAAATATGCTCTCTCAGAAA 1680
QY 1909 ACTATGGAATAGGGGAGAACTTAACATCTAGAACATTTAGATATACCGATTTTAGTAAT 1968
DB 1681 ACTATGGAATAGGGGAGAACTTAACATCTAGAACATTTAGATATACCGATTTTAGTAAT 1740
QY 1969 CTTTCTTCAATTTAGAGCTAATCCAGATATAATTTGGGATAAGTGAACAACCTCTATTTGT 2028
DB 1741 CTTTCTTCAATTTAGAGCTAATCCAGATATAATTTGGGATAAGTGAACAACCTCTATTTGT 1800
QY 2029 GCAGGTTCTTATAGTGGTGAACCTTTATATAGATAAAATTTGAAATTTATTTCTAGCAGAT 2088
DB 1801 GCAGGTTCTTATAGTGGTGAACCTTTATATAGATAAAATTTGAAATTTATTTCTAGCAGAT 1860
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Matches 1924; Conservative 0; Mismatches 508; Indels 51; Gaps 7;

QY	2089	GCAACATTTTGAAGCAGAACTCTGATTTTGAAGAGAGACAAAAGCGGTGAATGCGCTGTTT	2148
DB	1861	GCAACATTTTGAAGCAGAACTCTGATTTTGAAGAGAGACAAAAGCGGTGAATGCGCTGTTT	1920
QY	2149	ACTTCTTCCAAATCAATCGGTTAAATAAACCAGATGTGACGGAATATCATATGATCAAGTA	2208
DB	1921	ACTTCTTCCAAATCAATCGGTTAAATAAACCAGATGTGACGGAATATCATATGATCAAGTA	1980
QY	2209	TCCAATTTAGTGATGTTTATCAGATGAATTTTCTGCTGGATCAAAAGCAGAAATGTCC	2268
DB	1981	TCCAATTTAGTGATGTTTATCAGATGAATTTTCTGCTGGATCAAAAGCAGAAATGTCC	2040
QY	2269	GAGAAAGTCAAAACATGCGAGCGACTCAGTGATGAGCGGAATTTACTTCAGATCCAAAC	2328
DB	2041	GAGAAAGTCAAAACATGCGAGCGACTCAGTGATGAGCGGAATTTACTTCAGATCCAAAC	2100
QY	2329	TTTCAAGGGATCAATAGACAAACAGACCGGTGCTGGAGAGAGATGACAGATTTACCATC	2388
DB	2101	TTTCAAGGGATCAATAGACAAACAGACCGGTGCTGGAGAGAGATGACAGATTTACCATC	2160
QY	2389	CAAGGAGAGATGACGATTTTCAAGAGAAATACGTCACATACCGGGTACCGTTGATGAG	2448
DB	2161	CAAGGAGAGATGACGATTTTCAAGAGAAATACGTCACATACCGGGTACCGTTGATGAG	2220
QY	2449	TGCTATCCACGATTTTATATCAGAAAAATAGATGATCGAAATTTAAAGCTTTATACCGT	2508
DB	2221	TGCTATCCACGATTTTATATCAGAAAAATAGATGATCGAAATTTAAAGCTTTATACCGT	2280
QY	2509	TATGAATTTAGAGGGTATATCAGAGATGATCAAGACTTAGAGAAATCTATTTGATCGCGTAC	2568
DB	2281	TATGAATTTAGAGGGTATATCAGAGATGATCAAGACTTAGAGAAATCTATTTGATCGCGTAC	2340
QY	2569	AATGCAAAACAGGAATGTAATGTGCGAGGACCGGTTCTTATGGCGGCTTTTCAGCC	2628
DB	2341	AATGCAAAACAGGAATGTAATGTGCGAGGACCGGTTCTTATGGCGGCTTTTCAGCC	2400
QY	2629	CAAGTCCAAATCGGAAGTGTGCGAGACCGAATCGATGCGGCGCACACCTTTGAATGGAAT	2688
DB	2401	CAAGTCCAAATCGGAAGTGTGCGAGACCGAATCGATGCGGCGCACACCTTTGAATGGAAT	2460
QY	2689	CTGTATCTAGATTTCTTCTGCGAG 2711	
DB	2461	CTGTATCTAGATTTCTTCTGCGAG 2483	

RESULT 12
US-09-997-914-29
; Sequence 29, Application US/09997914
; Publication No. US20030119158A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; APPLICANT: Gilmer, Amy Jelen
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad Spectrum d-Endotoxins
; FILE REFERENCE: 11792.0215.DVUS01 MECO:215--1
; CURRENT APPLICATION NUMBER: US/09/997,914
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/261,040
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
US-09-997-914-29

Query Match 55.3%; Score 1498.2; DB 11; Length 3579;


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QY 1330 TTATCAATTCCTACTTTTACGATTTATTACAGCAACCTTGCAGCGCCACCACTTTTAATTTA 1389
DB 1081 ACATTTATCGTCACCTTTTATATAGAGACCTTTTAAATATAGGGATAAATAATCAACAAC 1140
QY 1390 CGTGGTGGTCAAGAGTAGAATTTCT- - - - -ACACCTACAATAGCTTTAG- - - - - 1437
DB 1141 TCTGTTCTTACCGGACAGAAATTTGCTTATGGAACTCTCCAAATTTGCCATCCGCTGTA 1200
QY 1438 TATGCAAGGAAGAGTACGGTGTGATTTCTTTAACTGAATTTACCGCTCAGGAGTAATAGTGTG 1497
DB 1201 TACAGAAAAGCGGACGGTAGATTTGCTGGATGAATATCCGACACAGATAACAAGTG 1260
QY 1498 CCACCTCGGAAAGGATATAGTCATCGTTTATGTATGTCATGCAACTTTTGTTC- - - - -AA 1548
DB 1261 CCACCTTAGGCAAGGATTTAGTCATCGAATTAAGCCATGTTTCAATGTTTCTGTCAGGCTTT 1320
QY 1549 AGATCTGGACACCTTTTAACTGATCCAGAGAGAAATTAATCAAAATACCTTTTAGTGAAGGATTT 1668
DB 1321 AGTAAATAGTAGTGAATTAATAGAGCTCTATGTTCTTTGGATACATCGTAGTGCA 1380
QY 1609 ACTCTTCAAAATACAATTCGATCCAGAGAGAAATTAATCAAAATACCTTTTAGTGAAGGATTT 1668
DB 1381 ACTCTTCAAAATACAATTCGATCCAGAGAGAAATTAATCAAAATACCTTTTAGTGAAGGATTT 1440
QY 1669 AGATTTGGGGGGGACCTCTGTCTATTACAGGACCAAGGATTTTACAGAGGGGATATCCTTT 1728
DB 1441 AGATTTGGGGGGGACCTCTGTCTATTACAGGACCAAGGATTTTACAGAGGGGATATCCTTT 1500
QY 1729 CGNAGAAATACCTTTGGTGAATTTGTTATCTCTACAGTCAATTAATTAATTCACCAATACC 1788
DB 1501 CGAAGAAATACCTTTGGTGAATTTGTTATCTCTACAGTCAATTAATTAATTCACCAATACC 1560
QY 1789 CAAAGATACCGTTTAAAGATTTGTTAGCTTCCAGTAGGATGACAGTATAGTATTA 1848
DB 1561 CAAAGATACCGTTTAAAGATTTGTTAGCTTCCAGTAGGATGACAGTATAGTATTA 1620
QY 1849 ACAGGACGGCATCCACAGAGTGGGAGGCCAAGTTAGTGTAGATATGCTCTTTCAGAAA 1908
DB 1621 ACAGGACGGCATCCACAGAGTGGGAGGCCAAGTTAGTGTAAATATGCTCTTCAGAAA 1680
QY 1909 ACTATGGAATAGGGAGAGACTTAACATCTAGAACATTTAGATATACCGATTTAGTAAT 1968
DB 1681 ACTATGGAATAGGGAGAGACTTAACATCTAGAACATTTAGATATACCGATTTAGTAAT 1740
QY 1969 CTTTTTTCATTTAGAGCTAATCCAGATATAATGGGATAAGTGAACACCTCTATTGCT 2028
DB 1741 CTTTTTTCATTTAGAGCTAATCCAGATATAATGGGATAAGTGAACACCTCTATTGCT 1800
QY 2029 GCAGGTTCTATTAGTAGCGTGAACCTTTATATAGATAAAATTTGAAATTTCTTAGCAGAT 2088
DB 1801 GCAGGTTCTATTAGTAGCGTGAACCTTTATATAGATAAAATTTGAAATTTCTTAGCAGAT 1860
QY 2089 GCAACATTTGAGAGCAATCTGATTTTAGAAGAGCAAAAAGCGGTGAATGCCCTGTTT 2148
DB 1861 GCAACATTTGAGAGCAATCTGATTTTAGAAGAGCAAAAAGCGGTGAATGCCCTGTTT 1920
QY 2149 ACTCTTCCAATCAATCGGTTTAAACCGATGTGACCGATTTATCATATTCATCAAGTA 2208
DB 1921 ACTCTTCCAATCAATCGGTTTAAACCGATGTGACCGATTTATCATATTCATCAAGTA 1980
QY 2209 TCCAAATTTAGTGGATTTGTTTATCAGATGAATTTTGTCTGGATGAAGAGGAGAAATTTGCC 2268
DB 1981 TCCAAATTTAGTGGATTTGTTTATCAGATGAATTTTGTCTGGATGAAGAGGAGAAATTTGCC 2040
QY 2269 GAGAAAGTCAAAATCGGAGCGACTCAGTGTATGAGCGGAATTTTACTTCAAGATCCAAAC 2328
DB 2041 GAGAAAGTCAAAATCGGAGCGACTCAGTGTATGAGCGGAATTTTACTTCAAGATCCAAAC 2100
QY 2329 TTCAGAGGATCAATAGACAAACGACCGTGGCTGGAGAGGAGTACAGATATTACCATC 2388
DB 2101 TTCAGAGGATCAATAGACAAACGACCGTGGCTGGAGAGGAGTACAGATATTACCATC 2160
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QY 2389 CAAGGAGGAGATGACGTAATTTCAAAGAGAAATTAAGTCACTACCGGTACCGTTGATGAG 2448
DB 2161 CAAGGAGGAGATGACGTAATTTCAAAGAGAAATTAAGTCACTACCGGTACCGTTGATGAG 2220
QY 2449 TCGTATCCAAACGTAATTTATATCAGAAAATAGATGAGTCAAAATTAAGCTTATACCCGT 2508
DB 2221 TCGTATCCAAACGTAATTTATATCAGAAAATAGATGAGTCAAAATTAAGCTTATACCCGT 2280
QY 2509 TATGAATTAAGAGGGTATATCAGAAATAGTCAAGACTTGAAGATCTTATTTGATCGGTAC 2568
DB 2281 TATGAATTAAGAGGGTATATCAGAAATAGTCAAGACTTGAAGATCTTATTTGATCGGTAC 2340
QY 2569 AATGCAAAACACGAAATAGTAAATGTGCCAGCAAGGTTCTTATGGCGCTTTTCAGCC 2628
DB 2341 AATGCAAAACACGAAATAGTAAATGTGCCAGCAAGGTTCTTATGGCGCTTTTCAGCC 2400
QY 2629 CAAAGTCCAATCGGAAGGTGCGAAGACCGAATCGATCGATCGCGCCACACCTTGAATGGAAT 2688
DB 2401 CAAAGTCCAATCGGAAGGTGCGAAGACCGAATCGATCGATCGCGCCACACCTTGAATGGAAT 2460
QY 2689 CCTGATCTAGATTTGTTCTTCGCGAG 2711
DB 2461 CCTGATCTAGATTTGTTCTTCGCGAG 2483
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RESULT 13

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US-10-365-645-29
; Sequence 29, Application US/10365645
; Publication No. US2003018282A1
; GENERAL INFORMATION:
; APPLICANT: Gilmer, Amy Jelen
; APPLICANT: Malvar, Thomas
; TITLE OF INVENTION: Antibodies Immunologically Reactive with Broad-Spectrum
; TITLE OF INVENTION: Delta-Endotoxins (Amended)
; FILE REFERENCE: 11792.0210.DVUS02 (MECO:210--3)
; CURRENT APPLICATION NUMBER: US/10/365,645
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: US 09/873,873
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 09/253,341
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 08/922,505
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
US-10-365-645-29
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Query Match 55.3%; Score 1498.2; DB 12; Length 3579;
Best Local Similarity 77.5%; Pred No. 1.1e-310;
Matches 1924; Conservative 0; Mismatches 508; Indels 51; Gaps 7;
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QY 259 AATCAATGCATACCTTACAATTTGTTTAAAGTAACTCTGAAGAGTACTTTTGGATGGAGAA 318
DB 22 AATGAATGCATTCCTTATAATTTGTTTAAAGTAACTCTGAAGTAAAGTATTAGTGGAGAA 81
QY 319 CGGATATCAACCTGGTAATTAATCTCTGTCTACTGTTCTGTTTCTGTTTCTGTTA 378
DB 82 AGAATAGAAACCTGGTTACACCCCAATCGATATTTCTTGTCTGCTAACCGAATTTCTTTTG 141
QY 379 TCTAACTTTGTACAGGGGGAGGATTTTGTAGTTAGTAAATAGATTTTGTATGGGGAATA 438
DB 142 AGTGAATTTGTTCCCGTGTCTGGATTTGTTAGGACTAGTTGATATAATATATGGGAAT 201
QY 439 GTTGCCCTCTCTCAATGGGATGCTATTTCTAGTACAAATTTGAACAATTAATTAATGAAGA 498
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Db 202 TTTGGTCCCTCTCAATGGGACGCAITTTCTGTACAAATTTGAACAGTAAATTAACCAAGA 261
Qy 499 ATAGCTGAATTTGCTAGGAATCTGCTATTGCTAATTTAGAAAGGATTTAGGAACAATTC 558
Db 262 ATAGAGAATTCGCTAGGACCAAGCAATTTCTAGATTAGAAAGGACTAAGCAATCTTTAT 321
Qy 559 AATATATATGTGGAGCAATTTAAAGAAATGGGAAGAGATCTTAATAATCCAGCAACGAG 618
Db 322 CAATTTAGCAGATCTTTAGAGAGTGGGAAGCAGATCCTACTAATCCAGCAATTAAGA 381
Qy 619 ACCAGATTAATGTACGCTTTCGTATCTGATGGCTACTTGAAGAGGACATTTCCCTTCG 678
Db 382 GAAGAGATCGTATTCATTCATGACATGACAGTGCCTTTACACCGCTATTTCTCTT 441
Qy. 679 TTTGCAATTTCTGGATTTGAAGTACCCCTTTTATCCGTTTATCTCTCAAGCGGCCAATCTG 738
Db 442 TTTGCAATTTCAAAATTTATCAAGTTCCTCTTTTACAGTATATGTTCAAGCTGCAAAATTA 501
Qy 739 CATCTAGCTATATTAAGAGATCTGTAAATTTTGGGAAGAGATTTGGATTTGACACGATA 798
Db 502 CAATTTATCAGTTTGAAGATGTTTCAGTGTGGACAAAGGTGGGATTTGATGCCGCG 561
Qy 799 AATGTCATGAAGAACTATATAAGACTAATTTAGGCGATTTGATGATGATGATGATGATG 858
Db 562 ACTATCAATAGTCTGTATAATGATTTAATCAGCTTTTATGGCACTATACAGATTTAGCT 621
Qy 859 GCAATACGTATTAATCGGGATTTAAATTAATTTACCGAATCTAGCTATCAAGATTTGATA 918
Db 622 GTACGCTGTACAAATACGGGATTTAGAACGTTATGGGACCGGATTTAGAGATTTGGTA 681
Qy 919 ACATATATCGATTTACGGAGAGCTTAACATGACGTATTTAGATATTCGCGCTTTCTT 978
Db 682 AGGTATTAATCAATTTAGAAAGAAATTAACACTAATGATTTAGATATTCGCTCTGTC 741
Qy 979 CCAAACTATGACAAATAGGAGATATCCAAATTCAGCCAGTTGGTCAACTAACAGAGGAT 1038
Db 742 CGGAATATGATAGTAGAAGATATCCAAATTCGAACAGTTTCCCAATTAACAGAGAAAT 801
Qy 1039 TATACGACCAATTAATTAATTTAATCCAGTTACAGTCTGTAGCTCAATTTACTACT 1098
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Qy 1099 TTTACGTTATGAGAGACGCAATTAGAAATCTCATTTATTTGATATTTGAATAT 1158
Db 847 TCGGCTCAGGCATAGAAAGAGTATTAGGAGTCCCAATTTGATGATTAATTAACAGT 906
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Db 907 ATAAACATCTATACGATGCTCATAGG-----GTTATTTATTTGCTCAGGCGCATCA 960
Qy 1219 GTAAATCTAGCCTTATAGG-----AGTGTAAACATAACATCTCTATATATGGAAGA 1272
Db 961 ATAAATGCTTCTCTGTAGGTTTTCGGGGCCAGAAATTCATTTTCGCTATATGGAAT 1020
Qy 1273 GAGCGAACCGAGGAGCTTCAAGATCTTTACTTTTAA---TGGACCGGTATTTAGGACT 1329
Db 1021 ATGGGAATGACGCTCCACAAACAAAGTATTTGCTCACTAGGTCAGGCGGTATAGA 1080
Qy 1330 TTATCAATCTCTATTTACGATTTATAGCAATTTGCTCCAGCGCCACATTTTAAATTA 1389
Db 1081 ACATATCTGCTCACTTTATATAGAGACCTTTTAAATAGGATTAATAACAACTA 1140
Qy 1390 CGTGTGTGTGAAGAGTATGAATTTCT-----ACACCTACAAATAGCTTTAG----- 1437
Db 1141 TCTGTCTTCTGTAGGAGACAGAAATTTGCTTATGGAACTCTCAATTTGCCATCCGCTGA 1200
Qy 1438 TATCGAGGAAGAGGTACGTTGATTTCTTTAATCTGATTTAGCTTACGCTCAGGATTAATGTG 1497
Db 1201 TACAGAAAGAGGAGACGCTGATTTGCTGGATGAATAACGCAAGATTAACAGCTG 1260
Qy 1498 CCACCTCGGAAGGATATAGTCATGCTTTATGTCAGCTTTTCTC-----AA 1548
Db 1261 CCACCTAGGACGAAATTTAGTCATGATTAAGCAATGTTTCAATGTTTCTGAGGCTTT 1320

Qy 1549 AGATCTGGAACACCTTTTAACTGCTGTAGTATTTTCTTGGACGCAATCTGTAGTGA 1608
Db 1321 AGTAATAGTAGTGAAGTATAATAAGAGCTCTCTATGTTCTCTTGGATACATCTGTAGTGA 1380
Qy 1609 ACTCTTACAAATACAAATTTGATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGGATTT 1668
Db 1381 ACTCTTACAAATACAAATTTGATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGGATTT 1440
Qy 1669 AGAGTTTGGGGGGGACCTCTCTGCTATTACAGAGCAGAGATTTACAGAGGGGATATCTCT 1728
Db 1441 AGAGTTTGGGGGGGACCTCTCTGCTATTACAGAGCAGAGATTTACAGAGGGGATATCTCT 1500
Qy 1729 CGAAGAAATACCTTTGCTGATTTTGTATCTCTCAAAAGTCAATTAATTAATCAACATTAAC 1788
Db 1501 CGAAGAAATACCTTTGCTGATTTTGTATCTCTCAAAAGTCAATTAATTAATCAACATTAAC 1560
Qy 1789 CAAAGATACCGTTTATAGATTTGCTTACGCTTCCAGTAGGGATGCGAGATTTAGTATTA 1848
Db 1561 CAAAGATACCGTTTATAGATTTGCTTACGCTTCCAGTAGGGATGCGAGATTTAGTATTA 1620
Qy 1849 ACAGAGCGGATCCACAGAGTGGGAGGCGCAAGTTAGTATATGCTCTTTCAGAAA 1908
Db 1621 ACAGAGCGGATCCACAGAGTGGGAGGCGCAAGTTAGTATATGCTCTTTCAGAAA 1680
Qy 1909 ACTATGGAATAAGGGGAGAACTTTAATCTAGACATTTAGTATATACCGATTTTAGTAA 1968
Db 1681 ACTATGGAATAAGGGGAGAACTTTAATCTAGACATTTAGTATATACCGATTTTAGTAA 1740
Qy 1969 CTTTTTTCATTTAGAGCTTAATCCAGATTAATTCGGATTAAGTGAACACCTCTATTGTT 2028
Db 1741 CTTTTTTCATTTAGAGCTTAATCCAGATTAATTCGGATTAAGTGAACACCTCTATTGTT 1800
Qy 2029 GCAGGTTCTATTTAGTACGTTGAACTTTATATAGATTAATAATTTGAATTTATCTAGCAG 2088
Db 1801 GCAGGTTCTATTTAGTACGTTGAACTTTATATAGATTAATAATTTGAATTTATCTAGCAG 1860
Qy 2089 GCAACATTTGAAGCAGAACTCTGATTTAGAAAGAGCAAAAGCGGTGAATGCTCTTT 2148
Db 1861 GCAACATTTGAAGCAGAACTCTGATTTAGAAAGAGCAAAAGCGGTGAATGCTCTTT 1920
Qy 2149 ACTTCTTCAATCAAACTCGGTTAAAAACCGATGTGACGATTTATCATATTGATCAAGTA 2208
Db 1921 ACTTCTTCAATCAAACTCGGTTAAAAACCGATGTGACGATTTATCATATTGATCAAGTA 1980
Qy 2209 TCCAAATTTAGTGGATTTGTTTATCAGATGAATTTTCTGATGAAAGCGGAAATTTGTC 2268
Db 1981 TCCAAATTTAGTGGATTTGTTTATCAGATGAATTTTCTGATGAAAGCGGAAATTTGTC 2040
Qy 2269 GAGAAAGTCAAACTGCGAAGCGACTCAGTGTAGCGGAAATTTTACTTCAAGATCCAAAC 2328
Db 2041 GAGAAAGTCAAACTGCGAAGCGACTCAGTGTAGCGGAAATTTTACTTCAAGATCCAAAC 2100
Qy 2329 TTCAGAGGATCAATAGACACCAAGACCGTGGCTGGAGAGGAGTACAGATATTACCATC 2388
Db 2101 TTCAGAGGATCAATAGACACCAAGACCGTGGCTGGAGAGGAGTACAGATATTACCATC 2160
Qy 2389 CAAGAGAGATGACGCTATTCAAGAGAAATTTAGCTCAGACTACCGGTACCGTGTAGTAG 2448
Db 2161 CAAGAGAGATGACGCTATTCAAGAGAAATTTAGCTCAGACTACCGGTACCGTGTAGTAG 2220
Qy 2449 TGTCTATCAACGTTATTTATTCAGAAATAGATGCTCGAAATTAAGAGCTTATACCGCT 2508
Db 2221 TGTCTATCAACGTTATTTATTCAGAAATAGATGCTCGAAATTAAGAGCTTATACCGCT 2280
Qy 2509 TATGAATTAAGAGGATTAATTCAGAGATGATAGAACTTAGAAATCTATTTGATCGGCTAC 2568
Db 2281 TATGAATTAAGAGGATTAATTCAGAGATGATAGAACTTAGAAATCTATTTGATCGGCTAC 2340
Qy 2569 AATGCAAAACAGAAATAGTAAATGTCGAGGACCGGTTCTTATGCGGCTTTTCAGCC 2628
Db 2341 AATGCAAAACAGAAATAGTAAATGTCGAGGACCGGTTCTTATGCGGCTTTTCAGCC 2400

QY 2629 CAAAGTCCAAATCGGAAGTGTGAGAACCGAATCGATGCGCGCCACACCTTGAATGGAAT 2688
DB 2401 CAAAGTCCAAATCGGAAGTGTGAGAACCGAATCGATGCGCGCCACACCTTGAATGGAAT 2460
QY 2689 CCTGATCTAGATGTTCTCTGCAG 2711
DB 2461 CCTGATCTAGATGTTCTCTGCAG 2483

RESULT 14
US-09-826-660-19
; Sequence 19, Application US/09826660
; Patent No. US2001002690A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven E.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 1860
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic B.t. toxin gene
US-09-826-660-19

Query Match 50.4%; Score 1366.2; DB 9; Length 1860;
Best Local Similarity 83.4%; Pred. No. 1.6e-282;
Matches 1551; Conservative 0; Mismatches 308; Indels 0; Gaps 0;

QY 241 ATGGAGGAAATTAATCAAAATCAATGCATACCTTCAATGTTTAAAGTAAATCTGAGAA 300
DB 1 ATGGAGGAGAAATCAAGATCAGTGCATACCTTCAATGTTTAAAGTAAATCTGAGAA 60
QY 301 GTACTTTTGGATGGAGAACCGATATCAACTGTTGTTTAAATGATATTTCTCTGTCA 360
DB 61 GTACTTTTGGATGGAGAACCGATATCAACTGTTGTTTAAATGATATTTCTCTGTCA 120
QY 361 CTGTGTTTCTGTATCTTAACTTTGTACAGGGGGAGGATTTTAAATGATATTTAAATA 420
DB 121 CTGTGTTTCTGTATCTTAACTTTGTACAGGGGGAGGATTTTAAATGATATTTAAATA 180
QY 421 GATTTGTTATGGGAATAGTGGCCCTTCTCAATGGGATGCAATTTCTAGTAAATGAA 480
DB 181 GATTTGTTATGGGCAATTTGGCCCATCTCAATGGGATGCAATTTCTAGTAAATGAA 240
QY 481 CAATTAATTAATGAAGAATAGTGAATTTGCTAGGAATGCTGATTTAAAGATTTAGAA 540
DB 241 CAGTTGATCAATGAGGAGTACTGAGTTTGTAGGAATGCTGCAATTTCCCAATCTGGA 300
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DB 421 GAAAGGCAATTCCTTCGTTTCGAAATTTCTGGAATTTGAGTACCCCTTCCTCCGTTGAT 480

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DB 541 TTGGGATTCACAAACGATATGTAATAAATGTAATAAATGTAATAAATGTAATAAATGTAATA 600
QY 841 GAAATATGCTGATCAGTGTGCAAAATAGTATAATCGGGGATTAATAAATTTTACCGAATCT 900
DB 601 GAGTATGCTGATCAGTGTGCAAAATAGTATAAATCGGGGATTAATAAATTTTACCGAATCT 660
QY 901 ACGTATCAAGATTTGGATAACATATATCGAATTCGGAGAGACTTAAATTCAGTGTGATTA 960
DB 661 ACGTATCAAGATTTGGATAACATATCGAATTCGGAGAGACTTAAATTCAGTGTGATTA 720
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QY 1141 TTTGATATATGAAATTAATCTTCAATCTTTTACGGAATTTGTTTGTGTTGAGAGCAATTTT 1200
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DB 1081 TTTAGGACTTTTCAATTTCTTACTTTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAAT 1140
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DB 1261 CCTCGGAAGGATATAGTCAATCTGTTTATGTAATGCAATTTTGTTCGAAAGTCTGGAACA 1320
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DB 1321 CGTTCCTGACAACTGTTGTTGTTTCTTCTGAGGCTTCTGAGTCACTTCACTTCACTTCACTT 1380
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DB 1381 ACCATTTGATCCAGAGAGGATCAATCAGATACCTTCTTGTGAAAGGCTTCAAGTTTGGGG 1440
QY 1681 GGCACCTCTGCTATTAAGGACCGAGATTTTACAGAGGGGATATCTTTCGAAAGAAATACC 1740
DB 1441 GGCACCTCTGCTATTAAGGACCGAGATTTTACAGAGGGGATATCTTTCGAAAGAAATACC 1500
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DB 1501 TTTGTTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1560
QY 1801 TTAAGATTTCTGTTTACGCTTCCAGTAGGATGTCAGCAGTTATATAGTATTAACAGGAGCGGCA 1860

Wed Oct 15 11:56:12 2003

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Qy	1861	TCCACAGAGGTGGAGGCGCAAGTTAGTGTAGATATGCTCTTTCAGAAAATATGGAATA	1920	333	TAATTAATGTTTAAAGTAACCCCTGAAGTAGAAGTATATTAGGTGGAGAAAGTAAGAAGCTGG	392
Db	1621	TCCACAGAGGTGGAGGCGCAAGTTAGTGTAGATATGCTCTTTCAGAAAATATGGAATA	1680	251	TTACACCCCAATCGATATTTCTTGTGCTGAAGCAATTTCTTTGAGTGAATTTGTTGCC	310
Qy	1921	GGGAGGAACTTAAACATCTAGAACATTTAGATATACCGATTTTAGTAATCTCTTTTCATT	1980	393	AGGGGAGGAACTTAAACATCTAGAACATTTAGATATACCGATTTTAGTAATCTCTTTTCATT	452
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Qy	1981	AGAGCTAATCCAGTAAATTTGGGTAAGTGAACAACTCTATTTGGTGGCAGGTTCTATT	2040	453	ATGGGATGCAATTTCTGTAGTACAAATTAATTAATCAAGAAATATGCTGAATTTGTC	512
Db	1741	AGAGCTAATCCAGTAAATTTGGGTAAGTGAACAACTCTATTTGGTGGCAGGTTCTATT	2099	371	ATGGGATGCAATTTCTGTAGTACAAATTAATTAATCAAGAAATATGCTGAATTTGTC	430
Qy	2041	AGTAGGCTTGAACCTTTATATAGTAAATTTGAATTTCTAGCAGATGCAACATTTGA	2099	513	TAGGATGCTGCTATTTGCTTTAGAGGATTTAGGAAACAAATTTCAATATATATGTGA	572
Db	1801	AGTAGGCTTGAACCTTTATATAGTAAATTTGAATTTCTAGCAGATGCAACATTTGA	1859	431	TAGGATGCTGCTATTTGCTTTAGAGGATTTAGGAAACAAATTTCAATATATATGTGA	490
RESULT 15						
US-09-756-643-1						
; Sequence 1, Application US/09756643						
; Patent No. US20010026939A1						
; GENERAL INFORMATION:						
; APPLICANT: Rice, Douglas						
; APPLICANT: Carozzi, Nadine						
; APPLICANT: Anderson, David						
; APPLICANT: Rajasekaran, Kanniah						
; APPLICANT: Rangan, Thirumale						
; APPLICANT: Yencofsky, Richard						
; APPLICANT: Lotstein, Richard						
; APPLICANT: De Framond, Annick						
; TITLE OF INVENTION: Insecticidal Cotton Plant Cells						
; FILE REFERENCE: S-16768E						
; CURRENT APPLICATION NUMBER: US/09/756.643						
; CURRENT FILING DATE: 2001-01-08						
; PRIOR APPLICATION NUMBER: 08/218,697						
; PRIOR FILING DATE: 1994-03-28						
; PRIOR APPLICATION NUMBER: 07/759,969						
; PRIOR FILING DATE: 1991-09-16						
; PRIOR APPLICATION NUMBER: 07/274,452						
; PRIOR FILING DATE: 1988-11-18						
; PRIOR APPLICATION NUMBER: 07/122,109						
; PRIOR FILING DATE: 1987-11-18						
; NUMBER OF SEQ ID NOS: 6						
; SOFTWARE: Patentin Ver. 2.0						
; SEQ ID NO 1						
; LENGTH 4360						
; TYPE: DNA						
; ORGANISM: Bacillus thuringiensis						
; FEATURE:						
; NAME/KEY: CDS						
; LOCATION: (156)..(3623)						
US-09-756-643-1						
Query Match						
Best Local Similarity						
Matches 1724; Conservative 0; Mismatches 780; Indels 78; Gaps 8;						
Qy	96	TGGGCAATATATGATATTTTATATAAATTTGTACGTTTGTATTTTTCATAAGATG	155	1173	GGATTTGTTTGTGTTGGAGCAATTTTATTTGGGAGGACATCGAGTAATATCTAGCCT	1232
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Qy	156	TGTCATATGATATAATCGTGTATGAAACAGTATCAACTATCAAGATTTGGTAG	215	1233	TATAGAGGTGGTAACTATCAATCTCTATATATGAAGAGGAGCAACAGAGGCTCC	1292
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Db	131	TTAATAAATAAAGAGATGAGGATTTTATGAGGAAAT---ATCAAAATCATCATACC	190	1196	ACACGATTTTGTCTCACTAGGTACAGGGGTGATGAACATATCTCTCTCACTTTATA	1255
Qy	273	TTAATAAATAAAGAGATGAGGATTTTATGAGGAAAT---ATCAAAATCATCATACC	332	1350	ATTATTAACAGCAACTTTGCCAGGCCACATTTTAAATTTACGTTGGTGGAGGAGTAGA	1409

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Db 1316 ATTTGCTTATGGAACCTCTCTCAAAATTTGCCATCGCTGTATACAGAAAAAGCGGACGGT 1375
Qy 1458 TGATTTCTTTAACTGAATACCGCTGAGGTAATAGTGTGCGACCTCGCGAAGAGATATAG 1517
Db 1376 AGATTGCGTGGATGAAATACCGCACAGAAATCAACGCTGCCACCTTAGGCAAGGATTTAG 1435
Qy 1518 TCATCGTTTATGTCATGCAACTTTTGTTCAA-----AGATCTGGAAACACCTTTTTT 1568
Db 1436 TCATCGATTAAGCCATGTTTCAATGTTTCTGTCAGGCTTTAGTAATAGTGTAGTAT 1495
Qy 1569 AACAACTGGTGTAGTATTTCTTGGACGCGATCGTAGTCAACTTTTACAATAACAATTGA 1628
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Qy 1629 TCAGAGAGAAATTAATCAAACTCTTAGTGAAGGATTTAGAGTTTGGGGGGCACCTC 1688
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Qy 1689 TGTCAATTACAGGACCAAGGATTTACAGAGGGGATATCTTCGAAGAATAACCTTTTGGTGA 1748
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Qy 1749 TTTTGTATCTCTACAAGTCAATTAATTAATCAACCAATTAACCAAGATACCTTTTAAAGATT 1808
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Qy 1809 TCGTTAGCTTCCAGTAGGGATGCGAGGATTAATAGTATTAACAGGAGCGGCATCCACAGG 1868
Db 1736 TCGCTACGCTTCTACCAAAATTTACAAT-----CCATACATC 1774
Qy 1869 AGTGGAGGCCAAGTTAGTGTAGATATGCTCTTCAGAAACTATGCAAACTAGGAATAGGGAGAA 1928
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Qy 1929 CTTAACATCTAGAACATTTAGATATACCGAATTTAGTAATCTTTTCAATTTAGAGCTAA 1988
Db 1835 TTTACAGTCCGGAAGCTTTAGGACTGTAGTTTACTCTCGTTTAACTTTTCAATGG 1894
Qy 1989 TCCAGATATAATTTGGGATTAAGTGAACAACCTCTATTTTGTGTCAGGTTCTTATAGTAGCT 2048
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Qy 2109 TGATTTAGAAAGAGCACAAAAGCGGTGAATGCCCTGTTTACTTCTTCCAATCAAAATCGG 2168
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Qy 2529 CGAAGATAGTCAAGACTTTAGAAATCTATTTGATCGGTTACAATGCAAAAACAGAAATAGT 2588
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Qy 2649 TG 2650
Db 2540 TG 2541

Search completed: October 13, 2003, 13:53:14
Job time : 2266 secs

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GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: October 9, 2003, 13:26:09 ; Search time 76 Seconds
(without alignments)
1744.851 Million cell updates/sec

Title: US-09-918-485-2

Perfect score: 4358

Sequence: 1 MEENNQICPIYNCLSNPBE.....GEPNRCAPLEWNPDLDCSC 823

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA.*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	4288	98.4	1189	11	US-09-972-175-2
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5	4287	98.4	1189	11	US-09-972-175-4
6	4283	98.3	1189	11	US-09-972-175-10
7	4282	98.3	1189	11	US-09-972-175-8
8	4282	98.3	1189	11	US-09-972-175-59
9	4281	98.2	1189	11	US-09-972-175-61
10	4111.5	94.3	1163	9	US-09-826-660-21
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12	3088	70.9	1193	11	US-09-977-914-10
13	3088	70.9	1193	12	US-10-365-645-30
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15	2537	58.2	1177	9	US-09-873-873-12

16	2537	58.2	1177	9	US-09-873-873-14
17	2537	58.2	1177	11	US-09-997-914-10
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25	2535	58.2	1177	12	US-10-365-645-26
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43	2334.5	53.6	1178	9	US-09-851-194-2
44	2266	52.0	1148	9	US-09-826-660-2
45	2264	52.0	1156	9	US-09-826-660-15

ALIGNMENTS

RESULT 1

US-09-918-485-2
; Sequence 2, Application US/09918485
; Publication No. US20030115628A1
; GENERAL INFORMATION:

APPLICANT: SANCHEZ, Vincent
LERECLOS, Didier
MENO, Ghislaine
LECADET, Marguerite-Marie
MARTOURET, Daniel
DREDONER, Raymond

TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR

POLYPEPTIDES ENDOWED WITH A LARVICIDAL ACTIVITY TOWARDS LEPIDOPTERA

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: USA

ZIP: 22313

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/918,485

FILING DATE: 25-Oct-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/461,551

FILING DATE: 05-JUN-1995

APPLICATION NUMBER: US 08/251,652

FILING DATE: 31-MAY-1994

APPLICATION NUMBER: US 07/458,754

FILING DATE: 11-DEC-1989

721 DVFKENYVTLFGTVDECYTYLYQKIDSKAYTRYELRGVIEDSDLEIYLIAYNAKH 780
721 DVFKENYVTLFGTVDECYTYLYQKIDSKAYTRYELRGVIEDSDLEIYLIAYNAKH 780
781 EIVNVPGTSLWPLSAQSPIGKGEFNRCAHLEWNPDLDCSC 823
781 EIVNVPGTSLWPLSAQSPIGKGEFNRCAHLEWNPDLDCSC 823

RESULT 2
US-09-972-175-12
Sequence 12, Application US/09972175
Publication No. US20030101482A1
GENERAL INFORMATION:
APPLICANT: Baum, James A.
Glimmer, Amy Jelen
Mectus, Anne-Marie Light
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,175
FILING DATE: 05-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/337,635
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-972-175-12

Query Match 98.4%; Score 4289; DB 11; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 MEENNQCIPYNCLEPVEVLDERISTGNSIDISLVQFLVSNFVPGGFLVGLI 60
DB 1 MEENNQCIPYNCLEPVEVLDERISTGNSIDISLVQFLVSNFVPGGFLVGLI 60
QY 61 DFVWGVGSPQWDAFLVQEQLINEARAEFARNAAIANLEGLGNFNIVYEAKEWEDP 120
DB 61 DFVWGVGSPQWDAFLVQEQLINEARAEFARNAAIANLEGLGNFNIVYEAKEWEDP 120
QY 121 NNPATRTVIDRFRILDLGLERDIPSPRISGFEVPLLSVYAAQANHLALRDSVIFGER 180
DB 121 NNPATRTVIDRFRILDLGLERDIPSPRISGFEVPLLSVYAAQANHLALRDSVIFGER 180
QY 181 WGLTTINVENNRLIRHIDEYADHCANTYNRGLNLPKSTYQDMITTYNRLRDLTLTVL 240
DB 181 WGLTTINVENNRLIRHIDEYADHCANTYNRGLNLPKSTYQDMITTYNRLRDLTLTVL 240
QY 241 DIAAFPNYDNRYPQVPQQLTREVTYDPLINFPQLQSVQALPTFNWESSAINPHL 300
DB 241 DIAAFPNYDNRYPQVPQQLTREVTYDPLINFPQLQSVQALPTFNWESSAINPHL 300
QY 301 FDLANNLTFTDWFSGRNFYMGHVRVSSLIIGGNITSPYIGREANQEPSPRFTNGVP 360
DB 301 FDLANNLTFTDWFSGRNFYMGHVRVSSLIIGGNITSPYIGREANQEPSPRFTNGVP 360
QY 361 FRTLSPTLRLLQPCORHFNLRGEGVEFSTPTNSFTYRGRGTVDLSITELPPEDNSVP 420
DB 361 FRTLSPTLRLLQPCORHFNLRGEGVEFSTPTNSFTYRGRGTVDLSITELPPEDNSVP 420
QY 421 PREGYSHRLCHATFVQSGTPTLTGGVFSWTHRSATLNTIDPERINQIPLVKGFRVWG 480
DB 421 PREGYSHRLCHATFVQSGTPTLTGGVFSWTHRSATLNTIDPERINQIPLVKGFRVWG 480
QY 481 GTSVITGPGFTGGDILRRNTFGDFVSLQVNSITQRYELFRYASSRDARVILTGAA 540
DB 481 GTSVITGPGFTGGDILRRNTFGDFVSLQVNSITQRYELFRYASSRDARVILTGAA 540
QY 541 STGVGQGVSNMPLQKTWEIGENLTSRFTYDTSNPFSEFRANPDIIIGSQPLFGAGSI 600
DB 541 STGVGQGVSNMPLQKTWEIGENLTSRFTYDTSNPFSEFRANPDIIIGSQPLFGAGSI 600
QY 601 SSGELYIDKIEIILADATFAESDLERAQKAVNALFTSSNQIGLTKTDVTHIDQVSNLV 660
DB 601 SSGELYIDKIEIILADATFAESDLERAQKAVNALFTSSNQIGLTKTDVTHIDQVSNLV 660
QY 661 DCLSDFECLDEKRELSEKVKHAKELSDERNLLQDNFPGINRQPDGRMGSTDTIIOGGD 720
DB 661 DCLSDFECLDEKRELSEKVKHAKELSDERNLLQDNFPGINRQPDGRMGSTDTIIOGGD 720

Db 181 WGLTTINVENYRLIRHIDEYADHCANTYNGLNLPKSTYQDWITYNRLRDLTLTVL 240
Qy 241 DIAAPPYNNRRYPIQPVQQLTRVYTDPLINFPQLQSVQALPTFNVMSSAIRNPHL 300
Db 241 DIAAPPYNNRRYPIQPVQQLTRVYTDPLINFPQLQSVQALPTFNVMSSAIRNPHL 300
Qy 301 FDLNNLTITFDWFSVGRNFWGHRVSSLIIGGNITSPIYGRANQPPRSFTNGPV 360
Db 301 FDLNNLTITFDWFSVGRNFWGHRVSSLIIGGNITSPIYGRANQPPRSFTNGPV 360
Qy 361 FRTLSTPLRLLOQPQRHFNLRGEGVEFSTPNSFTYGRGTVDLSITELPPEDNSVP 420
Db 361 FRTLSTPLRLLOQPQRHFNLRGEGVEFSTPNSFTYGRGTVDLSITELPPEDNSVP 420
Qy 421 PREGYSHRLCHATFVQSRGTPFTLTGTVFVSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
Db 421 PREGYSHRLCHATFVQSRGTPFTLTGTVFVSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
Qy 481 GTSVITGPGFTGGDILRRNTFGDFVSLQVNSPITQRYRLFRYASSRDARVILVTGAA 540
Db 481 GTSVITGPGFTGGDILRRNTFGDFVSLQVNSPITQRYRLFRYASSRDARVILVTGAA 540
Qy 541 STGVGQVSNVMPLOKTMELGENLTSTRTYTDPSNPFSPFRANPDIIGISEQPLFCAGSI 600
Db 541 STGVGQVSNVMPLOKTMELGENLTSTRTYTDPSNPFSPFRANPDIIGISEQPLFCAGSI 600
Qy 601 SSGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKTVDYHIDQVSNLV 660
Db 601 SSGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKTVDYHIDQVSNLV 660
Qy 661 DCLSDFCDEKRELSKVKHAKRLSDERNLQDPNFRGINRQPDGRWGSTDITIQGSD 720
Db 661 DCLSDFCDEKRELSKVKHAKRLSDERNLQDPNFRGINRQPDGRWGSTDITIQGSD 720
Qy 721 DVFKENYVTLPGTVDECPYLYQKIDESKUKATRYELRGYIEDSQDLEIYLIRYNAKH 780
Db 721 DVFKENYVTLPGTVDECPYLYQKIDESKUKATRYELRGYIEDSQDLEIYLIRYNAKH 780
Qy 781 EIVNVPGTGLWPLSAQSPIGKGEPNRCAPHLEWNPDLDCSC 823
Db 781 EIVNVPGTGLWPLSAQSPIGKGEPNRCAPHLEWNPDLDCSC 823

RESULT 3

US-09-972-175-2
; Sequence 2, Application US/09972175
; Publication No. US20030101482A1
; GENERAL INFORMATION:

; APPLICANT: Baum, James A.
; Gilmer, Amy Jelen
; Mettus, Anne-Marie Light
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
; LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,175
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/337,635
; FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MECO:206
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1189 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-09-972-175-2

Query Match 98.4%; Score 4288; DB 11; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 MEENNONCIPYNCILSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
Db 1 MEENNONCIPYNCILSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
Qy 61 DFVWGIVGPSQWDAFLVQIEQLINERIAEFAFARNAAIANLEGIGNNFNIYVEAFKEWEDP 120
Db 61 DFVWGIVGPSQWDAFLVQIEQLINERIAEFAFARNAAIANLEGIGNNFNIYVEAFKEWEDP 120
Qy 121 NNPATRTVIDRFRILDGLLDRIDPSFRISGEFVPLLSVYAAQANLHAILRDSVIFGBR 180
Db 121 NNPATRTVIDRFRILDGLLDRIDPSFRISGEFVPLLSVYAAQANLHAILRDSVIFGBR 180
Qy 181 WGLTTINVENYRLIRHIDEYADHCANTYNGLNLPKSTYQDWITYNRLRDLTLTVL 240
Db 181 WGLTTINVENYRLIRHIDEYADHCANTYNGLNLPKSTYQDWITYNRLRDLTLTVL 240
Qy 241 DIAAPPYNNRRYPIQPVQQLTRVYTDPLINFPQLQSVQALPTFNVMSSAIRNPHL 300
Db 241 DIAAPPYNNRRYPIQPVQQLTRVYTDPLINFPQLQSVQALPTFNVMSSAIRNPHL 300
Qy 301 FDLNNLTITFDWFSVGRNFWGHRVSSLIIGGNITSPIYGRANQPPRSFTNGPV 360
Db 301 FDLNNLTITFDWFSVGRNFWGHRVSSLIIGGNITSPIYGRANQPPRSFTNGPV 360
Qy 361 FRTLSTPLRLLOQPQRHFNLRGEGVEFSTPNSFTYGRGTVDLSITELPPEDNSVP 420
Db 361 FRTLSTPLRLLOQPQRHFNLRGEGVEFSTPNSFTYGRGTVDLSITELPPEDNSVP 420
Qy 421 PREGYSHRLCHATFVQSRGTPFTLTGTVFVSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
Db 421 PREGYSHRLCHATFVQSRGTPFTLTGTVFVSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
Qy 481 GTSVITGPGFTGGDILRRNTFGDFVSLQVNSPITQRYRLFRYASSRDARVILVTGAA 540
Db 481 GTSVITGPGFTGGDILRRNTFGDFVSLQVNSPITQRYRLFRYASSRDARVILVTGAA 540
Qy 541 STGVGQVSNVMPLOKTMELGENLTSTRTYTDPSNPFSPFRANPDIIGISEQPLFCAGSI 600
Db 541 STGVGQVSNVMPLOKTMELGENLTSTRTYTDPSNPFSPFRANPDIIGISEQPLFCAGSI 600
Qy 601 SSGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKTVDYHIDQVSNLV 660
Db 601 SSGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKTVDYHIDQVSNLV 660
Qy 661 DCLSDFCDEKRELSKVKHAKRLSDERNLQDPNFRGINRQPDGRWGSTDITIQGSD 720
Db 661 DCLSDFCDEKRELSKVKHAKRLSDERNLQDPNFRGINRQPDGRWGSTDITIQGSD 720
Qy 721 DVFKENYVTLPGTVDECPYLYQKIDESKUKATRYELRGYIEDSQDLEIYLIRYNAKH 780
Db 721 DVFKENYVTLPGTVDECPYLYQKIDESKUKATRYELRGYIEDSQDLEIYLIRYNAKH 780
Qy 781 EIVNVPGTGLWPLSAQSPIGKGEPNRCAPHLEWNPDLDCSC 823

us-09-918-485-2.rapb

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Db 781 EIVNPGTSLWPLSAQSPGKCGPNRCAPHLEWNPDLDCSC 823
RESULT 4
US-09-972-175-6
; Sequence 6, Application US/09972175
; Publication No. US20030101482A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; Gilmer, Amy Jelen
; Mettus, Anne-Marie Light
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
; LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,175
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/337,635
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MECO:206
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1189 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-972-175-6
Query Match 98.4%; Score 4288; DB 11; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 MEENNONQIPYNCISNPPEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
Db 1 MEENNONQIPYNCISNPPEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
Qy 61 DFVWGVGSPQWDAFLVQIEQLINERIAEFARNAIAANLEGLGNFNFIYVEAFKEWEDP 120
Db 61 DFVWGVGSPQWDAFLVQIEQLINERIAEFARNAIAANLEGLGNFNFIYVEAFKEWEDP 120
Qy 121 NNPAATRVIRDFRILDLIERDIPSRISGFEVPLISVAQAANLHLAIRDSDVIFGER 180
Db 121 NNPAATRVIRDFRILDLIERDIPSRISGFEVPLISVAQAANLHLAIRDSDVIFGER 180
Qy 181 MGLTTINVENYRLIRHIDEYADHCANTYRGLNLPKSTYQDWITYNRLRDLTLTVL 240
Db 181 MGLTTINVENYRLIRHIDEYADHCANTYRGLNLPKSTYQDWITYNRLRDLTLTVL 240
Qy 241 DIAAFPNYDNRYPPIQPVGQLTRVYTDLINFPQLQSVQALPTFNWESSAIRNPHL 300
Db 241 DIAAFPNYDNRYPPIQPVGQLTRVYTDLINFPQLQSVQALPTFNWESSAIRNPHL 300

Qy 301 FDIILNNLTFTDFSVGCRNFYWGHRVVISLIGGNITSTIYCRANOEPPRSFTENGVP 360
Db 301 FDIILNNLTFTDFSVGCRNFYWGHRVVISLIGGNITSTIYCRANOEPPRSFTENGVP 360
Qy 361 FRTLSIPTLRLLQPCQRHHFNLRGGEVGFSTPTNSGFTYRGRGTVDLSITELPEDNSVP 420
Db 361 FRTLSIPTLRLLQPCQRHHFNLRGGEVGFSTPTNSGFTYRGRGTVDLSITELPEDNSVP 420
Qy 421 PREGYSHRLCHATFVQRSQTPFLTGTGVFSWTHRSATLNTIDPERINOIPLVKGFRVWG 480
Db 421 PREGYSHRLCHATFVQRSQTPFLTGTGVFSWTHRSATLNTIDPERINOIPLVKGFRVWG 480
Qy 481 GTSVITGPGFTGGDILRRNTGDFVSLQVNNINSPIQYRLRFRFYASSRDARVILTGAA 540
Db 481 GTSVITGPGFTGGDILRRNTGDFVSLQVNNINSPIQYRLRFRFYASSRDARVILTGAA 540
Qy 541 STVGQGVSVNMPLOKTMWEIGENLTSTRTFYTDPSNPFSSFRANPDIIIGISEQLFAGSI 600
Db 541 STVGQGVSVNMPLOKTMWEIGENLTSTRTFYTDPSNPFSSFRANPDIIIGISEQLFAGSI 600
Qy 601 SSGELYDKIEILLADATFEASDLERAQAVNALFTSSNQIGLTKTDVTDYHIDQVSNLV 660
Db 601 SSGELYDKIEILLADATFEASDLERAQAVNALFTSSNQIGLTKTDVTDYHIDQVSNLV 660
Qy 661 DCLSDPCLDEKRELSEKVKHAKRLSDERNLLODPNFRGINRQPDGRWGSTDTITIQGD 720
Db 661 DCLSDPCLDEKRELSEKVKHAKRLSDERNLLODPNFRGINRQPDGRWGSTDTITIQGD 720
Qy 721 DVFKNYVTLPGTVDCEYTYLYOKIDSKLKAATRYELRGVIEDSOBLEIYLIYNAKH 780
Db 721 DVFKNYVTLPGTVDCEYTYLYOKIDSKLKAATRYELRGVIEDSOBLEIYLIYNAKH 780
Qy 781 EIVNPGTSLWPLSAQSPGKCGPNRCAPHLEWNPDLDCSC 823
Db 781 EIVNPGTSLWPLSAQSPGKCGPNRCAPHLEWNPDLDCSC 823
RESULT 5
US-09-972-175-4
; Sequence 4, Application US/09972175
; Publication No. US20030101482A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; Gilmer, Amy Jelen
; Mettus, Anne-Marie Light
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
; LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,175
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/337,635
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MECO:206
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1189 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-972-175-6

us-09-918-485-2.rapb

Wed Oct 15 11:56:19 2003

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QY 361 FRTLSIPTLRLLQOPCORHFNLRGEGVEFSTPTNSFTYRGRTVDSLTPELPPDNPV 420
Db 361 FRTLSIPTLRLLQOPCORHFNLRGEGVEFSTPTNSFTYRGRTVDSLTPELPPDNPV 420
QY 421 PRGYSHRLCHATFVQSGTPTFTTGVVFSWTHRSATLTNTIDPERINQIPLVKGRFVWG 480
Db 421 PRGYSHRLCHATFVQSGTPTFTTGVVFSWTHRSATLTNTIDPERINQIPLVKGRFVWG 480
QY 481 GTSVITGPGFTGDI LRNTFGDFVSLQVNSPITQYRLFRYASSRDARVILVTGAA 540
Db 481 GTSVITGPGFTGDI LRNTFGDFVSLQVNSPITQYRLFRYASSRDARVILVTGAA 540
QY 541 STGVGGQVSNMPLQKMEIGENLTSTRTYTDPSNPFSPRANPDIIIGISQPLFGAGSI 600
Db 541 STGVGGQVSNMPLQKMEIGENLTSTRTYTDPSNPFSPRANPDIIIGISQPLFGAGSI 600
QY 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLKTVDVTDVHIDQVSNLV 660
Db 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLKTVDVTDVHIDQVSNLV 660
QY 661 DCLSDFCDEKRELSKVKHAKLSDERNLLQDPNFRGINRQPDGRWGSDTITIQGD 720
Db 661 DCLSDFCDEKRELSKVKHAKLSDERNLLQDPNFRGINRQPDGRWGSDTITIQGD 720
QY 721 DVFKNYVTLPGFTVDECYPTLYQKIDESKLYATRYELGYIEDSDLEIYLAYNAKH 780
Db 721 DVFKNYVTLPGFTVDECYPTLYQKIDESKLYATRYELGYIEDSDLEIYLAYNAKH 780
QY 781 EIVNVPGTGLMPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
Db 781 EIVNVPGTGLMPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

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RESULT 7

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US-09-972-175-8
; Sequence 8, Application US/09972175
; Publication No. US20030101482A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
;           Mettus, Anne-Marie Light
;           Gilmer, Amy Jelen
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
;                     LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
;   ADDRESS: Arnold, White & Durkee
;   STREET: P. O. Box 4433
;   CITY: Houston
;   STATE: Texas
;   COUNTRY: USA
;   ZIP: 77210
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/972,175
;   FILING DATE: 05-Oct-2001
;   CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/337,635
;   FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: Kitchell, Barbara S.
;   REGISTRATION NUMBER: 33,928
;   REFERENCE/DOCKET NUMBER: WECO:206
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512/418-3000
;   TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 8:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1189 amino acids

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RESULT 8

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US-09-972-175-59
; Sequence 59, Application US/09972175
; Publication No. US20030101482A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-972-175-8
Query Match 98.3%; Score 4282; DB 11; Length 1189;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 812; Conservative 9; Mismatches 0; Gaps 0;
QY 1 MEENQNCIPYNCNPEVLLDGERISTGNSSIDISLSVQFLVNSFVPGGFLVGLI 60
Db 1 MEENQNCIPYNCNPEVLLDGERISTGNSSIDISLSVQFLVNSFVPGGFLVGLI 60
QY 61 DFWGIVGPSQDAFLVQIEQLINERIAEAPARNAALANLEGLGNFNFIYVEAFKEWEDP 120
Db 61 DFWGIVGPSQDAFLVQIEQLINERIAEAPARNAALANLEGLGNFNFIYVEAFKEWEDP 120
QY 121 NNPATRTVTRFRILDGILLERDIPSPRISGFVPLLSVYAAANLHLAILRDSVIFGER 180
Db 121 NNPATRTVTRFRILDGILLERDIPSPRISGFVPLLSVYAAANLHLAILRDSVIFGER 180
QY 181 WGLTTINNVNENYLRHIDEVADHCANTYNGLNLPKSTYQDMITYNRLRDLTLTVL 240
Db 181 WGLTTINNVNENYLRHIDEVADHCANTYNGLNLPKSTYQDMITYNRLRDLTLTVL 240
QY 241 DIAAFPNYDNRRTPIQVQGLTRVYTDPLINFPOLQSVQALPTFNWMESSAIRNPHL 300
Db 241 DIAAFPNYDNRRTPIQVQGLTRVYTDPLINFPOLQSVQALPTFNWMESSAIRNPHL 300
QY 301 FDIANNLTFTDWFSGVRNFYWGHRVSSLIIGCGNITSPYIGREANOEPPRSFTFNGPV 360
Db 301 FDIANNLTFTDWFSGVRNFYWGHRVSSLIIGCGNITSPYIGREANOEPPRSFTFNGPV 360
QY 361 FRTLSIPTLRLLQOPCORHFNLRGEGVEFSTPTNSFTYRGRTVDSLTPELPPDNPV 420
Db 361 FRTLSIPTLRLLQOPCORHFNLRGEGVEFSTPTNSFTYRGRTVDSLTPELPPDNPV 420
QY 421 PRGYSHRLCHATFVQSGTPTFTTGVVFSWTHRSATLTNTIDPERINQIPLVKGRFVWG 480
Db 421 PRGYSHRLCHATFVQSGTPTFTTGVVFSWTHRSATLTNTIDPERINQIPLVKGRFVWG 480
QY 481 GTSVITGPGFTGDI LRNTFGDFVSLQVNSPITQYRLFRYASSRDARVILVTGAA 540
Db 481 GTSVITGPGFTGDI LRNTFGDFVSLQVNSPITQYRLFRYASSRDARVILVTGAA 540
QY 541 STGVGGQVSNMPLQKMEIGENLTSTRTYTDPSNPFSPRANPDIIIGISQPLFGAGSI 600
Db 541 STGVGGQVSNMPLQKMEIGENLTSTRTYTDPSNPFSPRANPDIIIGISQPLFGAGSI 600
QY 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLKTVDVTDVHIDQVSNLV 660
Db 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLKTVDVTDVHIDQVSNLV 660
QY 661 DCLSDFCDEKRELSKVKHAKLSDERNLLQDPNFRGINRQPDGRWGSDTITIQGD 720
Db 661 DCLSDFCDEKRELSKVKHAKLSDERNLLQDPNFRGINRQPDGRWGSDTITIQGD 720
QY 721 DVFKNYVTLPGFTVDECYPTLYQKIDESKLYATRYELGYIEDSDLEIYLAYNAKH 780
Db 721 DVFKNYVTLPGFTVDECYPTLYQKIDESKLYATRYELGYIEDSDLEIYLAYNAKH 780
QY 781 EIVNVPGTGLMPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
Db 781 EIVNVPGTGLMPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

```

	Gilmer, Amy Jelen	
	Mettus, Anne-Marie Light	
	TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING	
	LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS	
	NUMBER OF SEQUENCES: 76	
	CORRESPONDENCE ADDRESS:	
	ADDRESSEE: Arnold, White & Durkee	
	STREET: P.O. Box 4433	
	CITY: Houston	
	STATE: Texas	
	COUNTRY: USA	
	ZIP: 77210	
	COMPUTER READABLE FORM:	
	MEDIUM TYPE: Floppy disk	
	COMPUTER: IBM PC compatible	
	OPERATING SYSTEM: PC-DOS/MS-DOS	
	SOFTWARE: PatentIn Release #1.0, Version #1.30	
	CURRENT APPLICATION DATA:	
	APPLICATION NUMBER: US/09/972,175	
	FILING DATE: 05-Oct-2001	
	CLASSIFICATION: <Unknown>	
	PRIOR APPLICATION DATA:	
	APPLICATION NUMBER: 09/337,635	
	FILING DATE: <Unknown>	
	ATTORNEY/AGENT INFORMATION:	
	NAME: Kitchell, Barbara S.	
	REGISTRATION NUMBER: 33,928	
	REFERENCE/DOCKET NUMBER: MECO:206	
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE: 512/418-3000	
	TELEFAX: 512/474-7577	
	INFORMATION FOR SEQ ID NO: 59:	
	SEQUENCE DESCRIPTION: SEQ ID NO: 59:	
	US-09-972-175-59	
	Query Match	98.3%; Score 4282; DB 11; Length 1189;
	Best Local Similarity	98.8%; Pred. No. 0;
	Matches 813; Conservative	0; Mismatches 10; Indels 0; Gaps 0;
QY	1 MEENNQCIPNCLSNPEVLLDGERISTGNSSIDISLVQFLVSNFVPGGFLVGLI	60
DB	1 MEENNQCIPNCLSNPEVLLDGERISTGNSSIDISLVQFLVSNFVPGGFLVGLI	60
QY	61 DFVGIVGPSQMDAFLVQEQLINERIAEFARNAAIANLEGNNFNYYEAPKEWEDP	120
DB	61 DFVGIVGPSQMDAFLVQEQLINERIAEFARNAAIANLEGNNFNYYEAPKEWEDP	120
QY	121 NNPAATRVDRFRILDLGLEDDIPSFRISGEVEPLLVSQAANLHAILRDSVFIFGR	180
DB	121 NNPAATRVDRFRILDLGLEDDIPSFAISGEVEPLLVSQAANLHAILRDSVFIFGR	180
QY	181 WGLTTINNENYNLRIRHIDEADHCANTYNGRLNLPKSTVDWTYNNRLRDDTLTVL	240
DB	181 WGLTTINNENYNLRIRHIDEADHCANTYNGRLNLPASTYQDWITTYNNRLRDDTLTVL	240
QY	241 DIAAFPPNYDNRRYPQPVGQLTREVTYDPLINFNPOLQSVAQLPTFNVMESSAIRNPHL	300
DB	241 DIAAFPPNYDNRRYPQPVGQLTREVTYDPLINFNPOLQSVAQLPTFNVMESSAIRNPHL	300
QY	301 FDLNLNLTFTDFWSVGRNFYGGHRVYSSLIGGNITSPIYGREANOEPFRSFTFNGPV	360
DB	301 FDLNLNLTFTDFWSVGRNFYGGHRVYSSLIGGNITSPIYGREANOEPFRSFTFNGPV	360
QY	361 FRTLSPTRLRLQQPCQRHHFNLRGGEGVEPRTPTNSFTYGRGVTDLSLTLPEDNSVP	420
DB	361 FRTLSPTRLRLQQCPWPAPPFWNLRGVGFVEFTPTNSFTYGRGVTDLSLTLPEDNSVP	420
QY	421 PREGYSHRLCHATFYQRSCTGPFLTGTGVVFSWTHRSATLTNTIDPERINQIPLVKGFVRWG	480

Wed Oct 15 11:56:19 2003

Query Match 98.2%; Score 4281; DB 11; Length 1189;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 813; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 MEENNONQICIPYNCISNPEVLLDGERISTGNSIDISLSVQFLVSNFVPGGFLVGLI 60
DB 1 MEENNONQICIPYNCISNPEVLLDGERISTGNSIDISLSVQFLVSNFVPGGFLVGLI 60
QY 61 DFVWGIVGSPQWDAFLVQIEQLINERIAEFARNAIAIANLEGNNFNIIYVEAFKEWDEEP 120
DB 61 DFVWGIVGSPQWDAFLVQIEQLINERIAEFARNAIAIANLEGNNFNIIYVEAFKEWDEEP 120
QY 121 NNPAATRVIDFRILDGLLERDIPSFRIISGFEVPLLSVYAAQAAHLAILRDSVIFGER 180
DB 121 NNPAATRVIDFRILDGLLERDIPSFRIISGFEVPLLSVYAAQAAHLAILRDSVIFGER 180
QY 181 WGLTTNNVENNRLIRHIDYADHCANTYNGLNLPKSTYQDMITYNRLRDLTLTVL 240
DB 181 WGLTTNNVENNRLIRHIDYADHCANTYNGLNLPKSTYQDMITYNRLRDLTLTVL 240
QY 241 DIAAFFPNYDNRRIPIQVQGLTREVVTDPLINFPOLQSVQALPTFNWMESSAIRNPHL 300
DB 241 DIAAFFPNYDNRRIPIQVQGLTREVVTDPLINFPOLQSVQALPTFNWMESSAIRNPHL 300
QY 301 FDIILNNLTFTDWFVSGRNFYWGHRVVISLIGGNITSPYIGREANQPFRSFTFNGPV 360
DB 301 FDIILNNLTFTDWFVSGRNFYWGHRVVISLIGGNITSPYIGREANQPFRSFTFNGPV 360
QY 361 FRTLSIPTLLLOQPCORHFNLRGEGVEFSTPTNSFTYGRGTVDLSLTLPEDNSVP 420
DB 361 FRTLSIPTLLLOQPCORHFNLRGEGVEFSTPTNSFTYGRGTVDLSLTLPEDNSVP 420
QY 421 PREGYSHRLCHATFVQSGTFLTTGVVFSWTHRSATLNTIDPERINQIPLVKGRVWG 480
DB 421 PREGYSHRLCHATFVQSGTFLTTGVVFSWTHRSATLNTIDPERINQIPLVKGRVWG 480
QY 481 GTSVITGPGTGGDILRRNTFCDFVLSQVQVNSPITQRYRLRYASSRDARVIVLTGAA 540
DB 481 GTSVITGPGTGGDILRRNTFCDFVLSQVQVNSPITQRYRLRYASSRDARVIVLTGAA 540
QY 541 STGVGGQVSNMPLQKTMIEIGENLTSTFRYTDSPNPFSSFRANPDIIIGISEQPLFAGSI 600
DB 541 STGVGGQVSNMPLQKTMIEIGENLTSTFRYTDSPNPFSSFRANPDIIIGISEQPLFAGSI 600
QY 601 SSGELYIDKIEIILADATFEASDLERAQAVNALFTSSNQIGLKTVDVTHIDQVSNLV 660
DB 601 SSGELYIDKIEIILADATFEASDLERAQAVNALFTSSNQIGLKTVDVTHIDQVSNLV 660
QY 661 DCLSEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINQPDGRWGSTDITIOGGD 720
DB 661 DCLSEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINQPDGRWGSTDITIOGGD 720
QY 721 DFKENYVTLPGTVDECYPTLYYQKIDESKLKATRYELRGYIEDSDLEIYLIYNAKH 780
DB 721 DFKENYVTLPGTVDECYPTLYYQKIDESKLKATRYELRGYIEDSDLEIYLIYNAKH 780

RESULT 10
US-09-826-660-21
Sequence 21, Application US/09826660
Patent No. US20010026940A1
GENERAL INFORMATION:
APPLICANT: Cardineau, Guy A.
APPLICANT: Stelman, Steven E.
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
FILE REFERENCE: MA-714XC2D1
CURRENT APPLICATION NUMBER: US/09/826,660

CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/178,252
PRIOR FILING DATE: 1998-10-23
PRIOR APPLICATION NUMBER: 60/065,215
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/076,445
PRIOR FILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 1163
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-21

Query Match 94.3%; Score 4111.5; DB 9; Length 1163;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 787; Conservative 8; Mismatches 23; Indels 5; Gaps 1;
QY 1 MEENNONQICIPYNCISNPEVLLDGERISTGNSIDISLSVQFLVSNFVPGGFLVGLI 60
DB 1 MEENNONQICIPYNCISNPEVLLDGERISTGNSIDISLSVQFLVSNFVPGGFLVGLI 60
QY 61 DFVWGIVGSPQWDAFLVQIEQLINERIAEFARNAIAIANLEGNNFNIIYVEAFKEWDEEP 120
DB 61 DFVWGIVGSPQWDAFLVQIEQLINERIAEFARNAIAIANLEGNNFNIIYVEAFKEWDEEP 120
QY 121 NNPAATRVIDFRILDGLLERDIPSFRIISGFEVPLLSVYAAQAAHLAILRDSVIFGER 180
DB 121 NNPAATRVIDFRILDGLLERDIPSFRIISGFEVPLLSVYAAQAAHLAILRDSVIFGER 180
QY 181 WGLTTNNVENNRLIRHIDYADHCANTYNGLNLPKSTYQDMITYNRLRDLTLTVL 240
DB 181 WGLTTNNVENNRLIRHIDYADHCANTYNGLNLPKSTYQDMITYNRLRDLTLTVL 240
QY 241 DIAAFFPNYDNRRIPIQVQGLTREVVTDPLINFPOLQSVQALPTFNWMESSAIRNPHL 300
DB 241 DIAAFFPNYDNRRIPIQVQGLTREVVTDPLINFPOLQSVQALPTFNWMESSAIRNPHL 300
QY 301 FDIILNNLTFTDWFVSGRNFYWGHRVVISLIGGNITSPYIGREANQPFRSFTFNGPV 360
DB 301 FDIILNNLTFTDWFVSGRNFYWGHRVVISLIGGNITSPYIGREANQPFRSFTFNGPV 360
QY 361 FRTLSIPTLLLOQPCORHFNLRGEGVEFSTPTNSFTYGRGTVDLSLTLPEDNSVP 420
DB 361 FRTLSIPTLLLOQPCORHFNLRGEGVEFSTPTNSFTYGRGTVDLSLTLPEDNSVP 420
QY 421 PREGYSHRLCHATFVQSGTFLTTGVVFSWTHRSATLNTIDPERINQIPLVKGRVWG 480
DB 421 PREGYSHRLCHATFVQSGTFLTTGVVFSWTHRSATLNTIDPERINQIPLVKGRVWG 480
QY 481 GTSVITGPGTGGDILRRNTFCDFVLSQVQVNSPITQRYRLRYASSRDARVIVLTGAA 540
DB 481 GTSVITGPGTGGDILRRNTFCDFVLSQVQVNSPITQRYRLRYASSRDARVIVLTGAA 540
QY 541 STGVGGQVSNMPLQKTMIEIGENLTSTFRYTDSPNPFSSFRANPDIIIGISEQPLFAGSI 600
DB 541 STGVGGQVSNMPLQKTMIEIGENLTSTFRYTDSPNPFSSFRANPDIIIGISEQPLFAGSI 600
QY 601 SSGELYIDKIEIILADATFEASDLERAQAVNALFTSSNQIGLKTVDVTHIDQVSNLV 660
DB 601 SSGELYIDKIEIILADATFEASDLERAQAVNALFTSSNQIGLKTVDVTHIDQVSNLV 660
QY 661 DCLSEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINQPDGRWGSTDITIOGGD 720
DB 661 DCLSEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINQPDGRWGSTDITIOGGD 720
QY 721 DFKENYVTLPGTVDECYPTLYYQKIDESKLKATRYELRGYIEDSDLEIYLIYNAKH 780
DB 721 DFKENYVTLPGTVDECYPTLYYQKIDESKLKATRYELRGYIEDSDLEIYLIYNAKH 780

QY 781 EIVNPGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823
Db 781 ETVNPGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 818

RESULT 11

US-09-873-873-30
; Sequence 30, Application US/09873873
; Patent No. US20020064865A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; APPLICANT: Gilmer, Amy Jelen
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins
; FILE REFERENCE: MECO:210--2
; CURRENT APPLICATION NUMBER: US/09/873,873
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 09/253,341
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 08/922,505
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 1193
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
US-09-873-873-30

Query Match 70.9%; Score 3088; DB 9; Length 1193;
Best Local Similarity 71.8%; Pred. No. 2.4e-283;
Matches 606; Conservative 68; Mismatches 132; Indels 38; Gaps 12;

QY 1 MEEN-NQOQIPYCNLSNPEEVLDDGERISTGSSIDISLSVQPLVSNFVPGGFLVGL 59
Db 1 MDNPNINECIPYCNLSNPEEVLDDGERISTGSSIDISLSVQPLVSNFVPGGFLVGL 60
QY 60 IDPVMGIVGPSOWDAFLVQIQLINERIAEFARNAANLEGLGNFNLYVEAFKEWEED 119
Db 61 VDIWIGIFGPSOWDAFLVQIQLINERIAEFARNAANLEGLGNFNLYVEAFKEWEED 120
QY 120 PNNPATRTRVIDRFDLGLDERDIPSRISGEFVEPLLSVYAQAANLHLAIRDSVIFGE 179
Db 121 PTNPALREEMRIQFNDMSALTATPLFAVQNYQVPLSVYQAANLHLVLRDVSFVQ 180
QY 180 RWGLTTINVENNRLIRHIDEYADHCANTYRGLNLPKSTYQDWITNRLRLDLTLTV 239
Db 181 RMGFDAATINSRYNDLTRIGNYTDYAVRWYNTGLERVMGPDSDRWVRYNQFRRELTIV 240
QY 240 LDIAAFPNYDNRYPYQVQGLTREYVTDPLI-NFNQLOQSVQALPTFNWMESSAIRNP 298
Db 241 LDIALFPNYSRRYPYQVQGLTREYVTDPLI-NFNQLOQSVQALPTFNWMESSAIRNP 299
QY 299 HLFDILNLTFTDWFSGRNFYWGHRVYSSLLIG--GGNITSPIYGREANOEPFRSFT- 355
Db 295 HLMDILNLTFTDWFSGRNFYWGHRVYSSLLIG--GGNITSPIYGREANOEPFRSFT- 352
QY 356 -FNGPVFRYLSIPTLLQOQCORHHFN-----LRGEGVEFSTPTN-----SFTYGR 403
Db 353 QLGGQYRTLS-----STLYRRPFTNIGNNQSLVLDGTEFAYGTSNLPSPAYVRS 404
QY 404 GTVDSLTLPBENSVPREGYSHRLCHATFVORSGTPTLTGVV-----FSWTHRSATLT 459
Db 405 GTVDSLTLPBENSVPREGYSHRLCHATFVORSGTPTLTGVV-----FSWTHRSATLT 463
QY 460 NTIDPERINQIPLVKGFRVWGTSVITGPGFTGGDILRRNTFGDFVSLQVWINSPIITORY 519
Db 464 NTIDPERINQIPLVKGFRVWGTSVITGPGFTGGDILRRNTFGDFVSLQVWINSPIITORY 523
QY 520 RLRFYASSRDARVILVTGAASTVGGQVSNMPLQKTMWEGENLTSTRTFRYTDPSNPFS 579

Db 524 RLRFYASSRDARVILVTGAASTVGGQVSNMPLQKTMWEGENLTSTRTFRYTDPSNPFS 583
QY 580 FRANPDIIGISROPLFGAGSISGELYIDKIEIILADATFEAESDLERAKAVNALFTSS 639
Db 584 FRANPDIIGISROPLFGAGSISGELYIDKIEIILADATFEAESDLERAKAVNALFTSS 643
QY 640 NOIGLKTVDYHIDQVSNLVCLSDFCLEKRELSKVGIAKRLSDERNLIQDPNFRG 699
Db 644 NOIGLKTVDYHIDQVSNLVCLSDFCLEKRELSKVGIAKRLSDERNLIQDPNFRG 703
QY 700 INRPDRGRGSTDITIQGDDVFKENYVTLTGTVDECYPTLYYQKIDSKLAKYTRYEL 759
Db 704 INRPDRGRGSTDITIQGDDVFKENYVTLTGTVDECYPTLYYQKIDSKLAKYTRYEL 763
QY 760 RGVIEDSQLEIYLYAYNAKHEIVNVPVGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDL 819
Db 764 RGVIEDSQLEIYLYAYNAKHEIVNVPVGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDL 823
QY 820 DCSC 823
Db 824 DCSC 827

RESULT 12

US-09-997-914-30
; Sequence 30, Application US/09997914
; Publication No. US20030119158A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; APPLICANT: Gilmer, Amy Jelen
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad Spectrum d-Endotoxins
; FILE REFERENCE: 11792.0215.DVUS01 MECO:215--1
; CURRENT APPLICATION NUMBER: US/09/997,914
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/261,040
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 1193
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
US-09-997-914-30

Query Match 70.9%; Score 3088; DB 11; Length 1193;
Best Local Similarity 71.8%; Pred. No. 2.4e-283;
Matches 606; Conservative 68; Mismatches 132; Indels 38; Gaps 12;

QY 1 MEEN-NQOQIPYCNLSNPEEVLDDGERISTGSSIDISLSVQPLVSNFVPGGFLVGL 59
Db 1 MDNPNINECIPYCNLSNPEEVLDDGERISTGSSIDISLSVQPLVSNFVPGGFLVGL 60
QY 60 IDPVMGIVGPSOWDAFLVQIQLINERIAEFARNAANLEGLGNFNLYVEAFKEWEED 119
Db 61 VDIWIGIFGPSOWDAFLVQIQLINERIAEFARNAANLEGLGNFNLYVEAFKEWEED 120
QY 120 PNNPATRTRVIDRFDLGLDERDIPSRISGEFVEPLLSVYAQAANLHLAIRDSVIFGE 179
Db 121 PTNPALREEMRIQFNDMSALTATPLFAVQNYQVPLSVYQAANLHLVLRDVSFVQ 180
QY 180 RWGLTTINVENNRLIRHIDEYADHCANTYRGLNLPKSTYQDWITNRLRLDLTLTV 239
Db 181 RMGFDAATINSRYNDLTRIGNYTDYAVRWYNTGLERVMGPDSDRWVRYNQFRRELTIV 240
QY 240 LDIAAFPNYDNRYPYQVQGLTREYVTDPLI-NFNQLOQSVQALPTFNWMESSAIRNP 298
Db 241 LDIALFPNYSRRYPYQVQGLTREYVTDPLI-NFNQLOQSVQALPTFNWMESSAIRNP 299

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QY	299	HLFDILNLTPTDWFVGRNFWGHRVVISLIG--CGNITSPYIGREANQPPRSFT-	355
Db	295	HLMDILNLTPTDWFVGRNFWGHRVVISLIG--CGNITSPYIGREANQPPRSFT-	352
QY	356	FNGPVRFLTSLPTLRLLQPCORHFN-----LRGGEVFEFTPTN-----SFTYRGR	403
Db	353	QLGQGVYRTLS-----STLYRRPFGNIGINNQQLSVLDGTEFAVGTSSNLPNAVYRKS	404
QY	404	GTVDLSLTPEDNSVPPREGYSHRLCHATFVQSGTPTFLTTGV-----FSWTHRSATLT	459
Db	405	GTVDLSLTPEDNSVPPREGYSHRLCHATFVQSGTPTFLTTGV-----FSWTHRSATLT	463
QY	460	NTIDPERINQIPLVKGFRVWGTSVITGPGTGGDILRRNTFGDFVSLQVINSPIQORY	519
Db	464	NTIDPERINQIPLVKGFRVWGTSVITGPGTGGDILRRNTFGDFVSLQVINSPIQORY	523
QY	520	RLRFRYASSRDARVILTGAASTGVGGQSVNMPLQKTMGEIGENLTSRFRYTDPSNPF	579
Db	524	RLRFRYASSRDARVILTGAASTGVGGQSVNMPLQKTMGEIGENLTSRFRYTDPSNPF	583
QY	580	FRANPDIIGISEQPLFGAGSISSGELYIDKIELIILADATFEASDLERAKAVNALFTSS	639
Db	584	FRANPDIIGISEQPLFGAGSISSGELYIDKIELIILADATFEASDLERAKAVNALFTSS	643
QY	640	NOIGLKTVDYHIDQVNLVDCLSDEFCLDEKRELSKVHAKRLSDERNLLQDPNFRG	699
Db	644	NOIGLKTVDYHIDQVNLVDCLSDEFCLDEKRELSKVHAKRLSDERNLLQDPNFRG	703
QY	700	INRQPDGRWGSDTITIOGGDDVFKNYVTLPGTVDECYPTLYQKIDSKLKAYTRYEL	759
Db	704	INRQPDGRWGSDTITIOGGDDVFKNYVTLPGTVDECYPTLYQKIDSKLKAYTRYEL	763
QY	760	RGYIEDSQDLEIYLIRYNAKHEIIVNVPFGTSLWPLSAQSPGKCGEPNRCAPHLEWPD	819
Db	764	RGYIEDSQDLEIYLIRYNAKHEIIVNVPFGTSLWPLSAQSPGKCGEPNRCAPHLEWPD	823
QY	820	DCSC 823	
Db	824	DCSC 827	
RESULT 14			
US-10-365-645-30			
; Sequence 30, Application US/10365645			
; Publication No. US20030182682A1			
; GENERAL INFORMATION:			
; APPLICANT: Malvar, Thomas			
; APPLICANT: Gilmer, Amy Jelen			
; TITLE OF INVENTION: Antibodies Immunologically Reactive with Broad-Spectrum			
; TITLE OF INVENTION: Delta-Endotoxins (Amended)			
; FILE REFERENCE: 11792.0210.DVUS02 (MECO:210--3)			
; CURRENT FILING DATE: 2003-02-12			
; PRIOR FILING DATE: 2001-06-04			
; PRIOR FILING DATE: 1999-02-19			
; PRIOR FILING DATE: 1997-09-03			
; PRIOR FILING DATE: 1996-11-20			
; NUMBER OF SEQ ID NOS: 35			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 30			
; LENGTH: 1193			
; TYPE: PRT			
; ORGANISM: Artificial			
; FEATURE:			
; OTHER INFORMATION: Hybrid Delta-Endotoxin			
US-10-365-645-30			
Query Match			
Best Local Similarity			
70.9%; Score 3088; DB 12; Length 1193;			
71.8%; Pred. No. 2.4e-283;			

Matches	606;	Conservative	68;	Mismatches	132;	Indels	38;	Gaps	12;
QY	1	MEEN-NONQICPYNCLSNPEEVLDDGERISTGNSSIDISLSVLQVFNVPVGGFLVGL	59						
Db	1	MDNNPINECIPYNCLSNPEEVLGGRIETGTPIDISLSTQFLSEFVPGAGFVLG	60						
QY	60	IDFVNGIVGSDQDAFLVOEQINERITAEFARNAAIANLEGLNNGNFIYVEAPKEWED	119						
Db	61	VDIINGIFGSDQDAFLVOEQINERITAEFARNAAIANLEGLNNGNFIYVEAFREWAD	120						
QY	120	PNNPATRFRVIDFRILDGLDERIDSPRISGEFEVLLSVYAAQANLHLAILEDVIFGE	179						
Db	121	PTNPALREEMRIQENDMSALTTATPLFAVQNTQVPLLSVYVQAAANLHLSLRDVSFVG	180						
QY	180	RKGLTIINVENNRILRIBHDEYADHCAVNTYRGLNANLPKSTVQDWITNRLRDLTLTV	239						
Db	181	RMGFDAATINRINDLRLTGLNYTDYAVRWNTGLERVWGPDSRDVRYNGFRELTTLV	240						
QY	240	LDIAAPFPYNNRRIPYPIQVQOLITREVTYDPLI-NENPOLQSVQALPTFNVMESSAIRNP	298						
Db	241	LDIALLFPYNNRRIPYPIQVQOLITREVTYDPLI-NENPOLQSVQALPTFNVMESSAIRNP	294						
QY	299	HLFDILNLTPTDWFVGRNFWGHRVVISLIG--CGNITSPYIGREANQPPRSFT-	355						
Db	295	HLMDILNLTPTDWFVGRNFWGHRVVISLIG--CGNITSPYIGREANQPPRSFT-	352						
QY	356	FNGPVRFLTSLPTLRLLQPCORHFN-----LRGGEVFEFTPTN-----SFTYRGR	403						
Db	353	QLGQGVYRTLS-----STLYRRPFGNIGINNQQLSVLDGTEFAVGTSSNLPNAVYRKS	404						
QY	404	GTVDLSLTPEDNSVPPREGYSHRLCHATFVQSGTPTFLTTGV-----FSWTHRSATLT	459						
Db	405	GTVDLSLTPEDNSVPPREGYSHRLCHATFVQSGTPTFLTTGV-----FSWTHRSATLT	463						
QY	460	NTIDPERINQIPLVKGFRVWGTSVITGPGTGGDILRRNTFGDFVSLQVINSPIQORY	519						
Db	464	NTIDPERINQIPLVKGFRVWGTSVITGPGTGGDILRRNTFGDFVSLQVINSPIQORY	523						
QY	520	RLRFRYASSRDARVILTGAASTGVGGQSVNMPLQKTMGEIGENLTSRFRYTDPSNPF	579						
Db	524	RLRFRYASSRDARVILTGAASTGVGGQSVNMPLQKTMGEIGENLTSRFRYTDPSNPF	583						
QY	580	FRANPDIIGISEQPLFGAGSISSGELYIDKIELIILADATFEASDLERAKAVNALFTSS	639						
Db	584	FRANPDIIGISEQPLFGAGSISSGELYIDKIELIILADATFEASDLERAKAVNALFTSS	643						
QY	640	NOIGLKTVDYHIDQVNLVDCLSDEFCLDEKRELSKVHAKRLSDERNLLQDPNFRG	699						
Db	644	NOIGLKTVDYHIDQVNLVDCLSDEFCLDEKRELSKVHAKRLSDERNLLQDPNFRG	703						
QY	700	INRQPDGRWGSDTITIOGGDDVFKNYVTLPGTVDECYPTLYQKIDSKLKAYTRYEL	759						
Db	704	INRQPDGRWGSDTITIOGGDDVFKNYVTLPGTVDECYPTLYQKIDSKLKAYTRYEL	763						
QY	760	RGYIEDSQDLEIYLIRYNAKHEIIVNVPFGTSLWPLSAQSPGKCGEPNRCAPHLEWPD	819						
Db	764	RGYIEDSQDLEIYLIRYNAKHEIIVNVPFGTSLWPLSAQSPGKCGEPNRCAPHLEWPD	823						
QY	820	DCSC 823							
Db	824	DCSC 827							
RESULT 14									
US-09-873-873-10									
; Sequence 10, Application US/09873873									
; Patent No. US20020064865A1									
; GENERAL INFORMATION:									
; APPLICANT: Malvar, Thomas									
; APPLICANT: Gilmer, Amy Jelen									
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins									
; FILE REFERENCE: MECO:210--2									
; CURRENT APPLICATION NUMBER: US/09/873,873									

; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 09/253,341
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 08/922,505
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 10
; LENGTH: 1177
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
US-09-873-873-10

Query Match 58.2%; Score 2537; DB 9; Length 1177;
Best Local Similarity 60.4%; Pred. No. 4.9e-231;
Matches 510; Conservative 92; Mismatches 191; Indels 52; Gaps 16;
QY 1 MEEN-NONOCIPYNCLSNPEEVLDDGERISTGSSIDISLSVQFLVSNFVPGGFLVGL 59
DB 1 MDNPNINECIPYNCLSNPEEVLGGERTGTPTIDISLQFLSEFVPGAGFVLGL 60
QY 60 IDFWGIVGPSOWDAFLVQIEQLINERIAEFARNAIAANLEGIGNNFNIYVEAFKEWEED 119
DB 61 VDIWIGIFGPSOWDAFLVQIEQLINERIAEFARNAIAANLEGIGNNFNIYVEAFKEWEED 120
QY 120 PNPATRTVIDRFRILDLGLLDERIDPSFRISGEVPLLSVYAAQANLHLAIRDVSIFGE 179
DB 121 PTNPALREEMRIQFNDMSALTTPALFAVQNYQVPLLSVYVQAANLHLAIRDVSIFGE 180
QY 180 RWGLTTINVENYNNRLIRHIDEYADHCANTYNGRLNLPKSTYQDWITYNRLRLDLTLV 239
DB 181 RWGFDAAATINSRNDLTRIGNTYDYAVRWYNTGLERWGPDSRDWRVNRQFRELTLV 240
QY 240 LDIAAFPPYNNRRYPIQVQLTREYVTDPLI-NFNQLOSVQAQPTFNVMESSAIRNP 298
DB 241 LDIALVFPYNNRRYPIQVQLTREYVTDPLI-NFNQLOSVQAQPTFNVMESSAIRNP 299
QY 299 HLPDIILNLTITFDWFSVGRNFWGCHRVISLIG--GNNITSPYIGREANQEPSPFT- 355
DB 295 HLMIDLINSITITVD--AHRGYVYWSGHQIMASPVGSGFEPFPLYGTMGNAAPQORIVA 352
QY 352 QLGQGVYRTLS-----STLYRRFPNIGINNQQLSVLDGTEFAFGTSSNLPNAVYRKS 404
QY 404 GTVDSLTELPPEDNSVPPREGYSHRLCHATFVQSGTFLTTGVV----FSWTHRSATLT 459
DB 405 GTVDSLDELIPQNNVPPRQGFHSRLSHVSMF-RSGFSNSSVSIIRAPMFSWTHRSATPT 463
QY 460 NTIDPRINQIPLVKGFRWGTGVTGTGFGDILRNTFGDVFVLSQVNNINSPIRORY 519
DB 464 NTIDPRITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGPFAYTTVINGQLPQRY 523
QY 520 RLRFVASSRDARVILVTCGAATGVGGVSVNMPLOKMTKEIGENTLSRTFRYTDPSNPES 579
DB 524 RARIRVASTINRIYV-TVAGERIFAGQ-----FNKTMDDTGDPLTFQSFYSATINTAPT 576
QY 580 FRANPDIIGISEQPLFGAGSISGG-ELYIDKIEIILADATFAESDLERAQKAVNALFTS 638
DB 577 FPMSSQSSFTV-----GADTFSSGNEVYIDRELIPVATFAEYDLERAQKAVNALFTS 630
QY 639 SNQIGLKTVDYHIDQVSNLVDCLSEFCLDEKRELSKVKHAKRLSDERNLLQDPNFR 698
DB 631 INQIGLKTVDYHIDQVSNLVDCLSEFCLDEKRELSKVKHAKRLSDERNLLQDPNFK 690
QY 699 GINRQDRGCRGSTDITIQGGDDVFKENYVTLPGTVDECPYLYOKIDESLKYATRYE 758
DB 691 GINRQLDRGCRGSTDITIQGGDDVFKENYVTLPGTFDBECYPLYLYOKIDESLKYATRYQ 750

QY 759 LRGYIEDSQDLREIYLAYNAKHEIVNVPGTGLWPLSAQSPICKGCEPNRCAPHLEWNP 818
DB 751 LRGYIEDSQDLREIYLIRYNAKHEIVNVPGTGLWPLSAQSPICKGCEPNRCAPHLEWNP 810
QY 819 LDCSC 823
DB 811 LDCSC 815
RESULT 15
US-09-873-873-12
; Sequence 12, Application US/09873873
; Patent No. US20020064865A1
; GENERAL INFORMATION:
; APPLICANT: Gilmer, Amy Jelen
; APPLICANT: Malvar, Thomas
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins
; FILE REFERENCE: MECO:210--2
; CURRENT APPLICATION NUMBER: US/09/873,873
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 09/253,341
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 08/922,505
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 12
; LENGTH: 1177
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
US-09-873-873-12

Query Match 58.2%; Score 2537; DB 9; Length 1177;
Best Local Similarity 60.4%; Pred. No. 4.9e-231;
Matches 510; Conservative 92; Mismatches 191; Indels 52; Gaps 16;
QY 1 MEEN-NONOCIPYNCLSNPEEVLDDGERISTGSSIDISLSVQFLVSNFVPGGFLVGL 59
DB 1 MDNPNINECIPYNCLSNPEEVLGGERTGTPTIDISLQFLSEFVPGAGFVLGL 60
QY 60 IDFWGIVGPSOWDAFLVQIEQLINERIAEFARNAIAANLEGIGNNFNIYVEAFKEWEED 119
DB 61 VDIWIGIFGPSOWDAFLVQIEQLINERIAEFARNAIAANLEGIGNNFNIYVEAFKEWEED 120
QY 120 PNPATRTVIDRFRILDLGLLDERIDPSFRISGEVPLLSVYAAQANLHLAIRDVSIFGE 179
DB 121 PTNPALREEMRIQFNDMSALTTPALFAVQNYQVPLLSVYVQAANLHLAIRDVSIFGE 180
QY 180 RWGLTTINVENYNNRLIRHIDEYADHCANTYNGRLNLPKSTYQDWITYNRLRLDLTLV 239
DB 181 RWGFDAAATINSRNDLTRIGNTYDYAVRWYNTGLERWGPDSRDWRVNRQFRELTLV 240
QY 240 LDIAAFPPYNNRRYPIQVQLTREYVTDPLI-NFNQLOSVQAQPTFNVMESSAIRNP 298
DB 241 LDIALVFPYNNRRYPIQVQLTREYVTDPLI-NFNQLOSVQAQPTFNVMESSAIRNP 299
QY 299 HLPDIILNLTITFDWFSVGRNFWGCHRVISLIG--GNNITSPYIGREANQEPSPFT- 355
DB 295 HLMIDLINSITITVD--AHRGYVYWSGHQIMASPVGSGFEPFPLYGTMGNAAPQORIVA 352
QY 352 QLGQGVYRTLS-----STLYRRFPNIGINNQQLSVLDGTEFAFGTSSNLPNAVYRKS 404
QY 404 GTVDSLTELPPEDNSVPPREGYSHRLCHATFVQSGTFLTTGVV----FSWTHRSATLT 459
DB 405 GTVDSLDELIPQNNVPPRQGFHSRLSHVSMF-RSGFSNSSVSIIRAPMFSWTHRSATPT 463
QY 460 NTIDPRINQIPLVKGFRWGTGVTGTGFGDILRNTFGDVFVLSQVNNINSPIRORY 519
DB 464 NTIDPRITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGPFAYTTVINGQLPQRY 523
QY 520 RLRFVASSRDARVILVTCGAATGVGGVSVNMPLOKMTKEIGENTLSRTFRYTDPSNPES 579
DB 524 RARIRVASTINRIYV-TVAGERIFAGQ-----FNKTMDDTGDPLTFQSFYSATINTAPT 576
QY 580 FRANPDIIGISEQPLFGAGSISGG-ELYIDKIEIILADATFAESDLERAQKAVNALFTS 638
DB 577 FPMSSQSSFTV-----GADTFSSGNEVYIDRELIPVATFAEYDLERAQKAVNALFTS 630
QY 639 SNQIGLKTVDYHIDQVSNLVDCLSEFCLDEKRELSKVKHAKRLSDERNLLQDPNFR 698
DB 631 INQIGLKTVDYHIDQVSNLVDCLSEFCLDEKRELSKVKHAKRLSDERNLLQDPNFK 690
QY 699 GINRQDRGCRGSTDITIQGGDDVFKENYVTLPGTVDECPYLYOKIDESLKYATRYE 758
DB 691 GINRQLDRGCRGSTDITIQGGDDVFKENYVTLPGTFDBECYPLYLYOKIDESLKYATRYQ 750

Wed Oct 15 11:56:19 2003

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Qy	520	RLRFRYASSRDARVIVLTGAASTGVGGQVSVNMPLQKMEIGENLTSRTFRYTDPSNPF	579
Db	524	RARIRVASTTNLRIVV-TVAGERIFAGQ-----FNKMTDGTGDLTTFQSFYATINTAFT	576
Qy	580	FRAMPDIIGISBQPLFGAGSISG-ELYIDKIEIILADATFEASDLERAQKAVNALFTS	638
Db	577	FPMQSQSFTV-----GADTFSGNEVYIDREFELIPVTATFEAYDLERAQKAVNALFTS	630
Qy	639	SNQIGLKTVDYHIDQVSNLVDCLSEFCLDEKRELSKVKHAKRLSDERNLLQDPNFR	698
Db	631	INQIGIKTDYHIDQVSNLVDCLSEFCLDEKRELSKVKHAKRLSDERNLLQDPNFK	690
Qy	699	GINQPDGRGSGTDITIQGGDDVFKENYVTLPGTVDECYPTLYQKIDESKLKAYTRYE	758
Db	691	GINQLDRGSGTDITIQGGDDVFKENYVTLPGTVDECYPTLYQKIDESKLKAFTRYQ	750
Qy	759	LRGVIEDSQLELYLIAYNAKHEIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNP	818
Db	751	LRGVIEDSQLELYLIAYNAKHEIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNP	810
Qy	819	LDCSC	823
Db	811	LDCSC	815

Search completed: October 9, 2003, 13:36:15
Job time : 80 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 13, 2003, 04:02:39 ; Search time 232 Seconds
(without alignments)
5157.714 Million cell updates/sec

Title: US-09-918-485-1
Perfect score: 2711
Sequence: 1 AAGCTCAATAGATCTCAA.....GATCTAGATTGTCCTGCAG 2711

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/prodata/2/ina/5A COMB.seq.*
2: /cgn2_6/prodata/2/ina/5B COMB.seq.*
3: /cgn2_6/prodata/2/ina/6A COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2711	100.0	2711	1	US-08-461-551-1
2	2711	100.0	2711	4	US-09-037-621A-1
3	2664	98.3	3223	4	US-08-465-609-4
4	2659.2	98.1	3223	3	US-09-176-320-7
5	2431	89.7	3567	1	US-08-602-737-1
6	2431	89.7	3567	3	US-09-001-982-1
7	2429.4	89.6	3567	1	US-07-828-788A-15
8	2429.4	89.6	3567	1	US-08-356-034-5
9	2429.4	89.6	3567	2	US-08-980-071-1
10	2429.4	89.6	3567	2	US-08-980-071-11
11	2429.4	89.6	3567	2	US-08-757-536-1
12	2429.4	89.6	3567	2	US-08-757-536-11
13	2429.4	89.6	3567	3	US-09-314-093-1
14	2429.4	89.6	3567	3	US-09-314-093-11
15	2429.4	89.6	3567	3	US-08-933-891-5
16	2429.4	89.6	3567	3	US-09-250-848-1
17	2429.4	89.6	3567	3	US-09-250-848-11
18	2429.4	89.6	3567	3	US-09-251-885-1
19	2429.4	89.6	3567	3	US-09-251-885-11
20	2429.4	89.6	3567	4	US-09-337-635-1
21	2429.4	89.6	3567	4	US-09-337-635-11
22	2429.4	89.6	3567	4	US-09-337-280-1
23	2429.4	89.6	3567	4	US-09-337-280-11
24	2429.4	89.6	3567	4	US-09-521-344-5
25	2429.4	89.6	3567	5	PCT-US92-11337-15
26	2429.4	89.6	3567	6	5188960-5
27	2427.8	89.6	3567	2	US-08-980-071-3

28 2427.8 89.6 3567 2 US-08-980-071-5 Sequence 5, Appli
29 2427.8 89.6 3567 2 US-08-980-071-9 Sequence 9, Appli
30 2427.8 89.6 3567 2 US-08-757-536-3 Sequence 3, Appli
31 2427.8 89.6 3567 2 US-08-757-536-5 Sequence 5, Appli
32 2427.8 89.6 3567 2 US-08-757-536-9 Sequence 9, Appli
33 2427.8 89.6 3567 3 US-09-314-093-3 Sequence 3, Appli
34 2427.8 89.6 3567 3 US-09-314-093-5 Sequence 5, Appli
35 2427.8 89.6 3567 3 US-09-314-093-9 Sequence 9, Appli
36 2427.8 89.6 3567 3 US-09-250-848-5 Sequence 5, Appli
37 2427.8 89.6 3567 3 US-09-250-848-9 Sequence 9, Appli
38 2427.8 89.6 3567 3 US-09-251-885-3 Sequence 3, Appli
39 2427.8 89.6 3567 3 US-09-251-885-5 Sequence 5, Appli
40 2427.8 89.6 3567 3 US-09-251-885-9 Sequence 9, Appli
41 2427.8 89.6 3567 4 US-09-337-635-3 Sequence 3, Appli
42 2427.8 89.6 3567 4 US-09-337-635-5 Sequence 5, Appli
43 2427.8 89.6 3567 4 US-09-337-635-9 Sequence 9, Appli
44 2427.8 89.6 3567 4 US-09-337-635-9 Sequence 9, Appli
45 2427.8 89.6 3567 4 US-09-337-280-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-08-461-551-1
; Sequence 1, Application US/08461551
; Patent No. 5792928
; GENERAL INFORMATION:
; APPLICANT: SANCHIS, Vincent
; APPLICANT: LERECLUS, Didier
; APPLICANT: MENOU, Ghislaine
; APPLICANT: LECADET, Marguerite-Marie
; APPLICANT: MARTOURET, Daniel
; APPLICANT: DEODONER, Raymond
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR
; TITLE OF INVENTION: POLYPEPTIDES ENDOWED WITH A LARVICIDAL ACTIVITY TOWARDS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,551
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,652
; FILING DATE: 31-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/458,754
; FILING DATE: 11-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 88 401 121.4
; FILING DATE: 06-MAY-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 87 08090
; FILING DATE: 10-JUN-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: HUNTINGTON, R. D.
; REGISTRATION NUMBER: 27,903
; REFERENCE/DOCKET NUMBER: 010830-073
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 1:									
SEQUENCE CHARACTERISTICS:									
LENGTH: 2711 base pairs									
TYPE: nucleic acid									
STRANDEDNESS: single									
TOPOLOGY: linear									
MOLECULE TYPE: DNA (genomic)									
US-08-461-551-1									
Query Match 100.0%; Score 2711; DB 1; Length 2711;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Db	1	AAGCTTCAATAGATCTCAAACTCTCGATGACTGCTTACTCTTTTAAATAGTCTCTACTTG	60						
Qy	61	ACAGGGGTAGGAACATAATCGGTCAATTTTAAATATGGGCGATATATCGATATTTTATAA	120						
Db	61	ACAGGGGTAGGAACATAATCGGTCAATTTTAAATATGGGCGATATATCGATATTTTATAA	120						
Qy	121	AAATTGTTAGCTTTTCTGTTATTTTTCATAAGATGTGTATATTAATTAATTAATTAATTA	180						
Db	121	AAATTGTTAGCTTTTCTGTTATTTTTCATAAGATGTGTATATTAATTAATTAATTAATTA	180						
Qy	181	TGAATAACAGTATCAAACTATCAGAACTTTGGTGTAGTTTAAATAAATAAATAAATAAATA	240						
Db	181	TGAATAACAGTATCAAACTATCAGAACTTTGGTGTAGTTTAAATAAATAAATAAATAAATA	240						
Qy	241	ATGAGGAAATATCAAACTATCAGAACTTTGGTGTAGTTTAAATAAATAAATAAATAAATA	300						
Db	241	ATGAGGAAATATCAAACTATCAGAACTTTGGTGTAGTTTAAATAAATAAATAAATAAATA	300						
Qy	301	GTACTTTGATGGGAAATAGTGGGCTTCTCAATGGGATGCAATTTAGTGTGATTAATA	360						
Db	301	GTACTTTGATGGGAAATAGTGGGCTTCTCAATGGGATGCAATTTAGTGTGATTAATA	360						
Qy	361	CTTGTTCAGTTTCTGTTATCTAATCTTGTATCCAGGGGAGGATTTTGTGATTAATA	420						
Db	361	CTTGTTCAGTTTCTGTTATCTAATCTTGTATCCAGGGGAGGATTTTGTGATTAATA	420						
Qy	421	GATTTTGTATGGGAAATAGTGGGCTTCTCAATGGGATGCAATTTAGTGTGATTAATA	480						
Db	421	GATTTTGTATGGGAAATAGTGGGCTTCTCAATGGGATGCAATTTAGTGTGATTAATA	480						
Qy	481	CAATTAATTAATGAAAGAAATAGTGGGCTTCTCAATGGGATGCAATTTAGTGTGATTA	540						
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Qy	541	GGATTAGGAAACAAATTTCAATATATATGTGGAAGCAATTTAAAGAAATGGGAAAGATCT	600						
Db	541	GGATTAGGAAACAAATTTCAATATATATGTGGAAGCAATTTAAAGAAATGGGAAAGATCT	600						
Qy	601	AATATCCAGCAACAGGACAGAGTAATTTGATCGCTTTTCTGATATGATGGGCTACTTT	660						
Db	601	AATATCCAGCAACAGGACAGAGTAATTTGATCGCTTTTCTGATATGATGGGCTACTTT	660						
Qy	661	GAAAGGACATCTCTGTTTCTGATTTCTGATTTTGAATGATCCCTTTTATCGTTTAT	720						
Db	661	GAAAGGACATCTCTGTTTCTGATTTTCTGATTTTGAATGATCCCTTTTATCGTTTAT	720						
Qy	721	GCTCAAGCGGCAATCTGATCTGATATATAGATTTCTGATTTTGAAGAAAGCA	780						
Db	721	GCTCAAGCGGCAATCTGATCTGATATATAGATTTCTGATTTTGAAGAAAGCA	780						
Qy	781	TTGGGATTCGACAGTAATATGATGAACTATTAATAGCTAATTTAGGCAATTTGAT	840						
Db	781	TTGGGATTCGACAGTAATATGATGAACTATTAATAGCTAATTTAGGCAATTTGAT	840						
Qy	841	GAATATGCTGATCACTGTGCAATATGATGCGGATTTAAATTTTACGGAATCT	900						
Db	841	GAATATGCTGATCACTGTGCAATATGATGCGGATTTAAATTTTACGGAATCT	900						

Qy	901	ACGTATCAAGATTGGATAACATATTAATCGATTACGAGAGACTTAACAATGACTGTATT	960
Db	901	ACGTATCAAGATTGGATAACATATTAATCGATTACGAGAGACTTAACAATGACTGTATT	960
Qy	961	GATATCGCGCTTTCTTCCAAATATGACAAATAGGAGATATCCAAATTCAGCCAGTTGGT	1020
Db	961	GATATCGCGCTTTCTTCCAAATATGACAAATAGGAGATATCCAAATTCAGCCAGTTGGT	1020
Qy	1021	CAACTAAACAGGGAAGTTTATACGACCCATTAATTAATTTTAAATCCACAGTTACAGTCT	1080
Db	1021	CAACTAAACAGGGAAGTTTATACGACCCATTAATTAATTTTAAATCCACAGTTACAGTCT	1080
Qy	1081	GTAGCTCAATTAACCTTCTTAACTTATGAGAGAGAGCAATTAGAAATCTCTCAATTTA	1140
Db	1081	GTAGCTCAATTAACCTTCTTAACTTATGAGAGAGAGCAATTAGAAATCTCTCAATTTA	1140
Qy	1141	TTTGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1200
Db	1141	TTTGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1200
Qy	1201	TATGGGAGGACATCGAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1260
Db	1201	TATGGGAGGACATCGAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1260
Qy	1261	ATATATGGAAGAGAGGCGAAACAGAGAGCTTCAAGATCTTTTAAATGAGCCGGTA	1320
Db	1261	ATATATGGAAGAGAGGCGAAACAGAGAGCTTCAAGATCTTTTAAATGAGCCGGTA	1320
Qy	1321	TTTAGGACTTTTATCAATTTCTTCTTAAATTAATTAATTAATTAATTAATTAATTAATTA	1380
Db	1321	TTTAGGACTTTTATCAATTTCTTCTTAAATTAATTAATTAATTAATTAATTAATTAATTA	1380
Qy	1381	TTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1440
Db	1381	TTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1440
Qy	1441	GCAGAGAGAGTACCGTTGATTCTTAACTGAAATTAATTAATTAATTAATTAATTAATTA	1500
Db	1441	GCAGAGAGAGTACCGTTGATTCTTAACTGAAATTAATTAATTAATTAATTAATTAATTA	1500
Qy	1501	CCTCGGAGGATATAGTATCGTTTATGTCATGCAATTTTGTTCATGAAATCTCTGGAACA	1560
Db	1501	CCTCGGAGGATATAGTATCGTTTATGTCATGCAATTTTGTTCATGAAATCTCTGGAACA	1560
Qy	1561	CTTTTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1620
Db	1561	CTTTTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1620
Qy	1621	ACAAATGATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGGATTTAGAGTTGGGG	1680
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Qy	1681	GGCACTCTGTCATTAACAGGAGGATTTACAGGAGGATATCTTTCGAGAAATACCC	1740
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Qy	1741	TTTGGTGAATTTGATCTCTCAAGTCAATTAATTAATTAATTAATTAATTAATTAATTAAT	1800
Db	1741	TTTGGTGAATTTGATCTCTCAAGTCAATTAATTAATTAATTAATTAATTAATTAATTAAT	1800
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Db	1801	TTAAGATTTCTGTTACGCTTCCAGTAGGATGAGAGGATTTAGTATTAACAGAGCGGCA	1860
Qy	1861	TCCAAGAGGATGGGAGGCGCAAGTTAGTATGATATGCTCTTTCAGAAATCTAGGAATA	1920
Db	1861	TCCAAGAGGATGGGAGGCGCAAGTTAGTATGATATGCTCTTTCAGAAATCTAGGAATA	1920
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Db	1921	GGGAGAGAACTTAACTATAGAAATTTAGATATACCGATTTTGTAGTATTTTCAATTT	1980
Qy	1981	AGAGCTAATCCAGATATTAATTTGGGATAGTGAACCACTCTATTTTGGTGCAGGTTCTATT	2040

1981 AGAGCTAATCCAGATATAATGGGTAAGTGAACAACCTCTATTTCGTGCGAGTCTATT 2040
2041 AGTAGCGTTGAACCTTTATATAGATAAAATGAAATTTATCTAGCAGATGCAACATTTGAA 2100
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2101 GCAGATCTGATTTAGAAAGAGACAAAGAGCGGTGAATGCCCTGTTTACTTCTTCCAAT 2160
2161 CAAATCGGTTAAACCCGATGACGGATATATATATGATCAAGTATCCCAATTTAGTG 2220
2161 CAAATCGGTTAAACCCGATGACGGATATATATATGATCAAGTATCCCAATTTAGTG 2220
2221 GATTGTTTATCAGATGAATTTGCTCTGGATGAAAGCGGAGAAATGTCGAGAAAGTCAAA 2280
2221 GATTGTTTATCAGATGAATTTGCTCTGGATGAAAGCGGAGAAATGTCGAGAAAGTCAAA 2280
2281 CATGGAAGCGACTAGTGATGAGCGGAATTTACTTTCAAGATCCAAACTTCAGAGGGATC 2340
2281 CATGGAAGCGACTAGTGATGAGCGGAATTTACTTTCAAGATCCAAACTTCAGAGGGATC 2340
2341 AATAGACAACACCGCTGGCTGGAGAGGAGTACAGATATTACCATCCAGAGGAGAT 2400
2341 AATAGACAACACCGCTGGCTGGAGAGGAGTACAGATATTACCATCCAGAGGAGAT 2400
2401 GAGCTATTCAAGAGAAATTTACGTACACTACCGGTGACCGTTGATGAGTCTTCAACG 2460
2401 GAGCTATTCAAGAGAAATTTACGTACACTACCGGTGACCGTTGATGAGTCTTCAACG 2460
2461 TATTTATATCAGAAATAGATGAGTCAAAATTTAAAGCTTATACCGCTTATGAATTAAGA 2520
2461 TATTTATATCAGAAATAGATGAGTCAAAATTTAAAGCTTATACCGCTTATGAATTAAGA 2520
2521 GGGTATATCGAAGATAGTCAAGCTTAGAAATCTATTGATCGCGTACAAACAC 2580
2521 GGGTATATCGAAGATAGTCAAGCTTAGAAATCTATTGATCGCGTACAAACAC 2580
2581 GAAATAGTAAATGTGCGAGCGGTTCTTATGCGCGCTTACGCCCAAAAGTCCAATC 2640
2581 GAAATAGTAAATGTGCGAGCGGTTCTTATGCGCGCTTACGCCCAAAAGTCCAATC 2640
2641 GGAAGTGTGGAAACCGAATCGATCGCGGCGCACACCTTTGAATGGAATCCTGATCTAGAT 2700
2641 GGAAGTGTGGAAACCGAATCGATCGCGGCGCACACCTTTGAATGGAATCCTGATCTAGAT 2700
2701 TGTTCCTGCAG 2711
2701 TGTTCCTGCAG 2711

RESULT 2
US-09-037-621A-1
Sequence 1, Application US/09037621A
Patent No. 6310035
GENERAL INFORMATION:
APPLICANT: SANCHIS, Vincent
LERECIUS, Didier
MENOUE, Ghislaine
LECADET, Marguerite-Marie
MARTOURET, Daniel
DEBONDER, Raymond
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR
POLYPEPTIDES ENDOWED WITH A LARVICIDAL ACTIVITY TOWARDS
LEPIDOPTERA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
City: Alexandria
STATE: Virginia
COUNTRY: USA

ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,621A
FILING DATE: 10-Mar-1998
CLASSIFICATION: <Unknown>
11-DEC-1989
06-MAY-1988
10-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,551
FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/459,754
FILING DATE: 11-DEC-1989
APPLICATION NUMBER: EP 88 401 121.4
FILING DATE: 06-MAY-1988
APPLICATION NUMBER: FR 87 08090
FILING DATE: 10-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: HUNTINGTON, R. D.
REGISTRATION NUMBER: 27,903
REFERENCE/DOCKET NUMBER: 010830-073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2711 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-037-621A-1

Query Match 100.0%; Score 2711; DB 4; Length 2711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCTTCAATAGAATCTCAAATCTCGATGACTGCTTAGTCTTTTAAATACGTCTACTTG 60
DB 1 AAGCTTCAATAGAATCTCAAATCTCGATGACTGCTTAGTCTTTTAAATACGTCTACTTG 60
QY 61 ACAGGGGTAGGAACATAATCGGTCAATTTTAAATATGGGCATATATTGATATTTTATAA 120
DB 61 ACAGGGGTAGGAACATAATCGGTCAATTTTAAATATGGGCATATATTGATATTTTATAA 120
QY 121 AATTGTTACGTTTTTGTATTTTTCATAGATGTCATATGTTTAAATCGTGTAA 180
DB 121 AATTGTTACGTTTTTGTATTTTTCATAGATGTCATATGTTTAAATCGTGTAA 180
QY 181 TGAATAACAGTATCAAACTATCAGAACTTTGTAGTCTTAAATAAAGGAGGTATTTT 240
DB 181 TGAATAACAGTATCAAACTATCAGAACTTTGTAGTCTTAAATAAAGGAGGTATTTT 240
QY 241 ATGGAGGAAATAATCAAAATCAATGCAATCCTTCAATGTTTAAAGTAATCCTGAAGAA 300
DB 241 ATGGAGGAAATAATCAAAATCAATGCAATCCTTCAATGTTTAAAGTAATCCTGAAGAA 300
QY 301 GTACTTTGGATGGAGACGATATCACTGTTTAAATGATATTTCTCTGTCA 360
DB 301 GTACTTTGGATGGAGACGATATCACTGTTTAAATGATATTTCTCTGTCA 360
QY 361 CTGTTTCAGTTTCTGTTATCTAACTTTTACAGGGGAGGATTTTGTAGTTGGATTAATA 420
DB 361 CTGTTTCAGTTTCTGTTATCTAACTTTTACAGGGGAGGATTTTGTAGTTGGATTAATA 420
QY 421 GATTTGTATGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATGAA 480

Db	421	GATTTGTATGGGGAATAGATTGGCCCTTCTCAATGGATCCATTTCTAGTACAAATTTGAA	480	1561	CCTTTTTTAAACAACCTGGTGTAGTATTTTCTTGGACGCGATCGTGTAGTGCACACTCTTACAAAT	1620
Qy	481	CAATTAATTAATGAAGAATAGCTGAATTTGCTTAGGAATCGTCTATTTGCTAAATTTAGAA	540	1561	CCTTTTTTAAACAACCTGGTGTAGTATTTTCTTGGACGCGATCGTGTAGTGCACACTCTTACAAAT	1620
Db	481	CAATTAATTAATGAAGAATAGCTGAATTTGCTTAGGAATCGTCTATTTGCTAAATTTAGAA	540	1621	ACAAATTTGATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGAGATTTTAGAGTTTGGGG	1680
Qy	541	GGATTAGGAAACAATTTCAATATATATGTGTGGAGCATTTAAGAAATGGGAGAGATCCT	600	1621	ACAAATTTGATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGAGATTTTAGAGTTTGGGG	1680
Db	541	GGATTAGGAAACAATTTCAATATATATGTGTGGAGCATTTAAGAAATGGGAGAGATCCT	600	1681	GGCACCTCTGTCAATTAACAGGACAGGATTTTACAGGAGGGGATATCTTTTGAAGAAATACC	1740
Qy	601	AATAATCCAGCAACAGGACAGAGTAATTTGATCGCTTTGTGTATCTTGTATGGGCTACTT	660	1681	GGCACCTCTGTCAATTAACAGGACAGGATTTTACAGGAGGGGATATCTTTTGAAGAAATACC	1740
Db	601	AATAATCCAGCAACAGGACAGAGTAATTTGATCGCTTTGTGTATCTTGTATGGGCTACTT	660	1741	TTTGGTGAATTTTGTATCTCTACAAAGTCAATTAATTAATTAATTAATTAATTAATTAATTAAT	1800
Qy	661	GAAGGGACATTTCTTCTGTTTCGAAATTTCTGGATTTGAAGTACCCCTTTTATTCGGTTTAT	720	1741	TTTGGTGAATTTTGTATCTCTACAAAGTCAATTAATTAATTAATTAATTAATTAATTAATTAAT	1800
Db	661	GAAGGGACATTTCTTCTGTTTCGAAATTTCTGGATTTGAAGTACCCCTTTTATTCGGTTTAT	720	1801	TTAAGATTTCCGTACGCTTCCAGTAGGATCGACAGTATATAGTATTAACAGGAGCGGCA	1860
Qy	721	GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTGGAGAAAGA	780	1801	TTAAGATTTCCGTACGCTTCCAGTAGGATCGACAGTATATAGTATTAACAGGAGCGGCA	1860
Db	721	GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTGGAGAAAGA	780	1861	TTCAAGGATTTGGGAGCGGCAAGTGTAGTATATGCTCTTCAGAAAACTATGAAATA	1920
Qy	781	TTGGGATTGACACGATAAATGTCAATGAAGTAACTATATAGACTTAATTAAGGATTTGAT	840	1861	TTCAAGGATTTGGGAGCGGCAAGTGTAGTATATGCTCTTCAGAAAACTATGAAATA	1920
Db	781	TTGGGATTGACACGATAAATGTCAATGAAGTAACTATATAGACTTAATTAAGGATTTGAT	840	1921	GGGGAGACTTAACATCTAGAACNTTTAGATATACCGATTTTAGTAATCCCTTTTCAATTT	1980
Qy	841	GAATATCTGCTACGCTGCGAATACGTATATTCGSGGATTAATTAATTTACCGAAATCT	900	1921	GGGGAGACTTAACATCTAGAACNTTTAGATATACCGATTTTAGTAATCCCTTTTCAATTT	1980
Db	841	GAATATCTGCTACGCTGCGAATACGTATATTCGSGGATTAATTAATTTACCGAAATCT	900	1981	AGAGCTAATCCAGATATAAATTTGGGATAGTGAACAACTCTATTTTGGTGGTCTTATTT	2040
Qy	901	ACGTATCAAGATTTGGATTAACATTAATTCGATTAACGAGAGACTTTAATTTGATCTGATTA	960	1981	AGAGCTAATCCAGATATAAATTTGGGATAGTGAACAACTCTATTTTGGTGGTCTTATTT	2040
Db	901	ACGTATCAAGATTTGGATTAACATTAATTCGATTAACGAGAGACTTTAATTTGATCTGATTA	960	2041	AGTAGCGTTGAACTTTATATAGATAAATTTGAAATTTTCTAGCAGATCAACATTTGAA	2100
Qy	961	GATATGCGCGCTTCTTCCAACTATGACATAGAGATTAACATTTAGCAGCTCGT	1020	2041	AGTAGCGTTGAACTTTATATAGATAAATTTGAAATTTTCTAGCAGATCAACATTTGAA	2100
Db	961	GATATGCGCGCTTCTTCCAACTATGACATAGAGATTAACATTTAGCAGCTCGT	1020	2101	CGAAATCTGATTTAGAAAGAGACACAAAAGCGGCTGAATGCGCTTTTACTTTCTCCAAAT	2160
Qy	1021	CAACTTAACAGGAGAGTTTATACGGACCCATTAATTTTATCAAGTTACAGTCACT	1080	2101	CGAAATCTGATTTAGAAAGAGACACAAAAGCGGCTGAATGCGCTTTTACTTTCTCCAAAT	2160
Db	1021	CAACTTAACAGGAGAGTTTATACGGACCCATTAATTTTATCAAGTTACAGTCACT	1080	2161	CAATCGGGTTAAAAACCGATGTGACGGATTTATCATATTTGATCAAGTATCCAAATTTAGTG	2220
Qy	1081	GTAGCTCAATTTACCTACTTTTAAAGTTATGAGAGAGCGCAATTTAGAAATCTCATTTA	1140	2161	CAATCGGGTTAAAAACCGATGTGACGGATTTATCATATTTGATCAAGTATCCAAATTTAGTG	2220
Db	1081	GTAGCTCAATTTACCTACTTTTAAAGTTATGAGAGAGCGCAATTTAGAAATCTCATTTA	1140	2221	GATTTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGAGAAATTTGTCGAGAGAAAGTCAAA	2280
Qy	1141	TTTGATATATTGAATATCTTACCAATCTTTTACCGATTTGTTAGTGTGACCAATTTT	1200	2221	GATTTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGAGAAATTTGTCGAGAGAAAGTCAAA	2280
Db	1141	TTTGATATATTGAATATCTTACCAATCTTTTACCGATTTGTTAGTGTGACCAATTTT	1200	2281	CATCGAAGCGACTCAGTGTAGCGGAATTTTACTTTCAAGATCCAAATTTTCAAGAGGATC	2340
Qy	1201	TATTTGGGAGGACATCGAGTAATATCTAGCCTTATAGGAGTGTGTAACATCTCTCT	1260	2281	CATCGAAGCGACTCAGTGTAGCGGAATTTTACTTTCAAGATCCAAATTTTCAAGAGGATC	2340
Db	1201	TATTTGGGAGGACATCGAGTAATATCTAGCCTTATAGGAGTGTGTAACATCTCTCTCT	1260	2341	AAATAGACACCCAGACCGCTGGCTGGAGAGGAGTACAGATATTTACCATCCAAAGGAGAGAT	2400
Qy	1261	ATATATGGAAGAGGAGGACCAAGGAGCTTCAAGATCTTTTACTTTTAAATGACCGGTA	1320	2341	AAATAGACACCCAGACCGCTGGCTGGAGAGGAGTACAGATATTTACCATCCAAAGGAGAGAT	2400
Db	1261	ATATATGGAAGAGGAGGACCAAGGAGCTTCAAGATCTTTTACTTTTAAATGACCGGTA	1320	2401	GACGTATTTCAAGAGAAATTTGCTACACTACCGGTACCGTTGATGAGTCTTATCCAAAG	2460
Qy	1321	TTTAGGACTTTTCAATTTCTTATAGATTTATACGACACCTTTGCGAGCGCAACAT	1380	2401	GACGTATTTCAAGAGAAATTTGCTACACTACCGGTACCGTTGATGAGTCTTATCCAAAG	2460
Db	1321	TTTAGGACTTTTCAATTTCTTATAGATTTATACGACACCTTTGCGAGCGCAACAT	1380	2461	TATTTATATCAGAAAAATAGATGAGTCCAAATTTAAGCTTATACCCGTATGAATTAAGA	2520
Qy	1381	TTTAAATTTACGTTGGTGGAGGAGTGAATTTTCTACACCTACAAATAGCTTTAGTAT	1440	2461	TATTTATATCAGAAAAATAGATGAGTCCAAATTTAAGCTTATACCCGTATGAATTAAGA	2520
Db	1381	TTTAAATTTACGTTGGTGGAGGAGTGAATTTTCTACACCTACAAATAGCTTTAGTAT	1440	2521	GGGTATATCGAAGATAGTCAAGATTTAGAAATCTTATTTGATCGCTCAATTCGCAACAC	2580
Qy	1441	GCAGGAGGAGTACGTTGATTTTAACTGAATTTACCGCTGAGGATTAATGAGTGTGCA	1500	2521	GGGTATATCGAAGATAGTCAAGATTTAGAAATCTTATTTGATCGCTCAATTCGCAACAC	2580
Db	1441	GCAGGAGGAGTACGTTGATTTTAACTGAATTTACCGCTGAGGATTAATGAGTGTGCA	1500	2581	GAATATAGTAAATGTCGAGGCAAGGTTCTTATGCGCTTTTATGCGCTTTTATGCGCTTTT	2640
Qy	1501	CCTCGGAGGAGTATAGTCAATCGTTTATGCTCAATGCACTTTTGTCAAGATCTGGAACA	1560	2581	GAATATAGTAAATGTCGAGGCAAGGTTCTTATGCGCTTTTATGCGCTTTTATGCGCTTTT	2640
Db		CCTCGGAGGAGTATAGTCAATCGTTTATGCTCAATGCACTTTTGTCAAGATCTGGAACA	1560			

QY 2641 GGAACTGTGGAGACCGAATCGATCGCGCCACACCTTGAATGGATCTGTATAGAT 2700
Db 2641 GGAAAGTGTGGAGACCGAATCGATCGCGCCACACCTTGAATGGATCTGTATAGAT 2700
QY 2701 TGTTCCTGCAG 2711
Db 2701 TGTTCCTGCAG 2711

RESULT 3

US-08-465-609-4
; Sequence 4, Application US/08465609
; Patent No. 5866784
; GENERAL INFORMATION:
; APPLICANT: Van Mellaert, Herman
; APPLICANT: Botterman, Johan
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Joos, Henk
; TITLE OF INVENTION: PREVENTION OF Bt RESISTANCE DEVELOPMENT
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: The George Mason Building, Washington &
; STREET: Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,609
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,274
; FILING DATE:
; APPLICATION NUMBER: US 07/640,400
; FILING DATE: 22-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: P36,113
; REFERENCE/DOCKET NUMBER: 010830-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; TELEX: 440580
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3923 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 234..3803
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..233
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 3804..3923
US-08-465-609-4

Query Match 98.3%; Score 2664; DB 2; Length 3923;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 2679; Conservative 25; Indels 0; Gaps 0;

QY

8 AATAGAATCTCAATCTCGATGACTGCTTAGTCTTTTAAATAGTCTGTACTTGGACAGGGG 67

Db 1 AATAGAATCTCAATCTCGATGACTGCTTAGTCTTTTAAATAGTCTGTACTTGGACAGGGG 60
QY 68 TAGGAACATAAATCGGTCAATTTTAAATATGGGCGATATATGATATTTTATAAAATTTGT 127
Db 61 TAGGAACATAAATCGGTCAATTTTAAATATGGGCGATATATGATATTTTATAAAATTTGT 120
QY 128 TAGGTTTTTGTATTTTTCATAAAGATGTCTCATATGTAATAAATCGTGTAAATGAAAAA 187
Db 121 TAGGTTTTTGTATTTTTCATAAAGATGTCTCATATGTAATAAATCGTGTAAATGAAAAA 180
QY 188 CAGTATCAAACTATCAGAACTTTTGTAGTTTAAATAAAAAACGGAGGTATTTTATCGAGG 247
Db 181 CAGTATCAAACTATCAGAACTTTTGTAGTTTAAATAAAAAACGGAGGTATTTTATCGAGG 240
QY 248 AAAATAATCAAAATCAATGATACCTTACAAATGTTTAAAGTAATCTCTGAAGAAGTACTTT 307
Db 241 AAAATAATCAAAATCAATGATACCTTACAAATGTTTAAAGTAATCTCTGAAGAAGTACTTT 300
QY 308 TGGATGGAGAACGGATATCAACTGGTAAATTAATCAATTGATATTTCTCTGTCACTTTGTTTC 367
Db 301 TGGATGGAGAACGGATATCAACTGGTAAATTAATCAATTGATATTTCTCTGTCACTTTGTTTC 360
QY 368 AGTTTCTGTATCTAACTTTGTACAGGGGGAGGATTTTGTAGTTGGAATTAATAGATTTTG 427
Db 361 AGTTTCTGTATCTAACTTTGTACAGGGGGAGGATTTTGTAGTTGGAATTAATAGATTTTG 420
QY 428 TATGGGAATAGTTGCGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTTGAACAATTA 487
Db 421 TATGGGAATAGTTGCGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTTGAACAATTA 480
QY 488 TTAATGAAAGATAGTCTGAATTTGCTAGGAATGCTGCTATTTGCTAAATTTAGAGGATTAG 547
Db 481 TTAATGAAAGATAGTCTGAATTTGCTAGGAATGCTGCTATTTGCTAAATTTAGAGGATTAG 540
QY 548 GAAACAATTTCAATATATATGTTGAAGCAATTTAAAGAATGGGAAGAGATCTTAATAATC 607
Db 541 GAAACAATTTCAATATATATGTTGAAGCAATTTAAAGAATGGGAAGAGATCTTAATAATC 600
QY 608 CAGCAACAGGACAGAGTAATTTGATCGTTTCGTATACCTTGATCGGCTACTTGAAGAGG 667
Db 601 CAGCAACAGGACAGAGTAATTTGATCGTTTCGTATACCTTGATCGGCTACTTGAAGAGG 660
QY 668 ACATTCCTTTCGTTTCGAAATTTCTGGATTTGAAGTACCCCTTTTATCCGTTTATGCTCAAG 727
Db 661 ACATTCCTTTCGTTTCGAAATTTCTGGATTTGAAGTACCCCTTTTATCCGTTTATGCTCAAG 720
QY 728 CGGCCAATCTGCATCTAGCTATATTAAGAGATCTGTAAATTTTTCGGAGAGAGATTTGGGAT 787
Db 721 CGGCCAATCTGCATCTAGCTATATTAAGAGATCTGTAAATTTTTCGGAGAGAGATTTGGGAT 780
QY 788 TGACAACGATAAATGTCATGAAACTATATAGACTAATTAGGCATATTTGATGAATATG 847
Db 781 TGACAACGATAAATGTCATGAAACTATATAGACTAATTAGGCATATTTGATGAATATG 840
QY 848 CTGATCACTGTGCAAAATACGTATATCGGGATTTAAATAAATTTACCGAAATCTAGCTATC 907
Db 841 CTGATCACTGTGCAAAATACGTATATCGGGATTTAAATAAATTTACCGAAATCTAGCTATC 900
QY 908 AAGATTGGATAACATATAATCGATTACCGAGAGACTTAACATTGATCTGTATTTAGATATCG 967
Db 901 AAGATTGGATAACATATAATCGATTACCGAGAGACTTAACATTGATCTGTATTTAGATATCG 960
QY 968 CGGCTTTCTTTCCAAACTATGCAATAGGAGATATCCAAATTTAGCCAGTTGGTCAACTAA 1027
Db 961 CGGCTTTCTTTCCAAACTATGCAATAGGAGATATCCAAATTTAGCCAGTTGGTCAACTAA 1020
QY 1028 CAAGGAAGTTTATACGGACCCATTAAATTTAAATTTTAAATCCACAGTTACAGTCTGTAGCTC 1087
Db 1021 CAAGGAAGTTTATACGGACCCATTAAATTTTAAATTTTAAATCCACAGTTACAGTCTGTAGCTC 1080
QY 1088 AATTAACCTACTTTTAAACGTTATGGAGAGACGCGCAATTTAGAAATCTCATTTTATTGATA 1147

Db	1081	AATTACCTCTTTAAACGTTATGAGAGCAGCGCAATTAGAAATCTCAATTTATTGATA	1140
Qy	1148	TATTGAATATCTTTAAACGTTATGAGAGCAGCGCAATTAGAAATCTCAATTTATTGATA	1207
Db	1141	TATTGAATATCTTTAAACGTTATGAGAGCAGCGCAATTAGAAATCTCAATTTATTGATA	1200
Qy	1208	GAGGACATCGAGTAATATCTAGCGTTATAGGAGTGGTACATACATCTCTATATAG	1267
Db	1201	GAGGACATCGAGTAATATCTAGCGTTATAGGAGTGGTACATACATCTCTATATAG	1260
Qy	1268	GAAGAGAGCGAACCAGGAGCTCCAAAGATCTCTTTTAAATGAGCGGTATTTAGGA	1327
Db	1261	GAAGAGAGCGAACCAGGAGCTCCAAAGATCTCTTTTAAATGAGCGGTATTTAGGA	1320
Qy	1328	CTTTTATCAATCTCTTATGAGTATTTACAGCAACCTTGCCAGCGCCACCACTTTAAT	1387
Db	1321	CTTTTATCAATCTCTTATGAGTATTTACAGCAACCTTGCCAGCGCCACCACTTTAAT	1380
Qy	1388	TACGTGGTGGTGAAGGAGTAGAATTTTCTACACCTACCAATAGCTTTAGCTATGAGGA	1447
Db	1381	TACGTGGTGGTGAAGGAGTAGAATTTTCTACACCTACCAATAGCTTTAGCTATGAGGA	1440
Qy	1448	GAGGTACGTTGATCTTTAACTGAATTTACCGCTGAGGATAATAGTGTGCCACCTCGCG	1507
Db	1441	GAGGTACGTTGATCTTTAACTGAATTTACCGCTGAGGATAATAGTGTGCCACCTCGCG	1500
Qy	1508	TACGTGGTGGTGAAGGAGTAGAATTTTCTACACCTACCAATAGCTTTAGCTATGAGGA	1567
Db	1501	TACGTGGTGGTGAAGGAGTAGAATTTTCTACACCTACCAATAGCTTTAGCTATGAGGA	1560
Qy	1568	TACGTGGTGGTGAAGGAGTAGAATTTTCTACACCTACCAATAGCTTTAGCTATGAGGA	1627
Db	1561	TACGTGGTGGTGAAGGAGTAGAATTTTCTACACCTACCAATAGCTTTAGCTATGAGGA	1620
Qy	1628	ATCCAGAGAGATTAATCAATACCTTTAGTGAAGGATTTAGTGTGGGGGGCACT	1687
Db	1621	ATCCAGAGAGATTAATCAATACCTTTAGTGAAGGATTTAGTGTGGGGGGCACT	1680
Qy	1688	CTGTCAATACAGGACAGGATTTACAGAGGGATCTCTCGAAGAAATACCTTTGGT	1747
Db	1681	CTGTCAATACAGGACAGGATTTACAGAGGGATCTCTCGAAGAAATACCTTTGGT	1740
Qy	1748	ATTTGTATCTCTCAAGTCAATATTAATTCACCAATACCCCAAGATACCTTTAGAT	1807
Db	1741	ATTTGTATCTCTCAAGTCAATATTAATTCACCAATACCCCAAGATACCTTTAGAT	1800
Qy	1808	TTCTGTACGCTTCCAGTAGGATGACAGGATTAATTAATTAACAGAGCGGATCCACG	1867
Db	1801	TTCTGTACGCTTCCAGTAGGATGACAGGATTAATTAATTAACAGAGCGGATCCACG	1860
Qy	1868	GAGTGGAGGCGCAAGTTAGTGTAGATATGCTCTTCAGAAAATAGGAGGAGA	1927
Db	1861	GAGTGGAGGCGCAAGTTAGTGTAGATATGCTCTTCAGAAAATAGGAGGAGA	1920
Qy	1928	ACTTAACATCTAGAACATTTAGATATACCGATTTTATGATCTCTTTTCAATTTAGAGCTA	1987
Db	1921	ACTTAACATCTAGAACATTTAGATATACCGATTTTATGATCTCTTTTCAATTTAGAGCTA	1980
Qy	1988	ATCCAGATATATTTGGATTAAGTGAACACCTCTATTTGGTGGAGGATCTTATAGTAGCG	2047
Db	1981	ATCCAGATATATTTGGATTAAGTGAACACCTCTATTTGGTGGAGGATCTTATAGTAGCG	2040
Qy	2048	TTCAACTTTATATAGATAAAATTTAAATTTATTTAGCAGATGCAACATTTGAAGCAGAT	2107
Db	2041	TTCAACTTTATATAGATAAAATTTAAATTTATTTAGCAGATGCAACATTTGAAGCAGAT	2100
Qy	2108	CTGATTTAGAGAGCAGCAAAAGCGGTGAATGCCCTGTTTACTCTTCCCAATCAATG	2167
Db	2101	CTGATTTAGAGAGCAGCAAAAGCGGTGAATGCCCTGTTTACTCTTCCCAATCAATG	2160
Qy	2168	GTTTAAAAACCGATGACGATTTATCATTTAGTCAAGTATCCATTTAGTGGATGTT	2227
Db	2161	GTTTAAAAACCGATGACGATTTATCATTTAGTCAAGTATCCATTTAGTGGATGTT	2220

RESULT 4

US-09-176-320-7
 ; Sequence 7, Application US/09176320
 ; Patent No. 6172281
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Mellaert, Herman
 ; APPLICANT: Botterman, Johan
 ; APPLICANT: Van Rie, Jeroen
 ; APPLICANT: Joos, Henk
 ; TITLE OF INVENTION: PREVENTION OF BT RESISTANCE DEVELOPMENT
 ; FILE REFERENCE: 021565-052
 ; CURRENT APPLICATION NUMBER: US/09/176,320
 ; EARLIER FILING DATE: 1998-10-22
 ; EARLIER APPLICATION NUMBER: PCT/EP90/00905
 ; EARLIER FILING DATE: 1990-05-30
 ; EARLIER APPLICATION NUMBER: GB 89401499.2
 ; EARLIER FILING DATE: 1989-05-31
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 3923
 ; TYPE: DNA
 ; ORGANISM: Bacillus thuringiensis
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (234)..(3803)
 ; US-09-176-320-7
 Query Match 98.1%; Score 2659.2; DB 3; Length 3923;
 Best Local Similarity 99.0%; Pred. No. 0;
 Matches 2676; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
 Qy 8 AATAAGATCTCAATCTCGATGCTGCTAGTCTTTTAACTCTCTTACTTCTACTTGCACAGGG 67
 Db 1 AATAAGATCTCAATCTCGATGCTGCTAGTCTTTTAACTCTCTTACTTCTACTTGCACAGGG 60

QY 68 TAGGAACATAAATCGGTCAATTTTAAATATATGGGCAATATATGTATATTTTATATAAAATTTGT 127
DB 61 TAGGAACATAAATCGGTCAATTTTAAATATATGGGCAATATATGTATATTTTATATAAAATTTGT 120
QY 128 TAGCTTTTGTATTTTTCATAAGATGTCTATATGATTAATAATCGTGTAAATGAATAA 187
DB 121 TAGCTTTTGTATTTTTCATAAGATGTCTATATGATTAATAATCGTGTAAATGAATAA 180
QY 188 CAGTATCAAACTATCAGAACTTTTGGTAGTTTAAATAAAAAAAGAGGTATTTTATGGAGG 247
DB 181 CAGTATCAAACTATCAGAACTTTTGGTAGTTTAAATAAAAAAAGAGGTATTTTATGGAGG 240
QY 248 AAAATAATCAAAATCAATGATACCTTACAAATTTGTTTAAAGTAAATCCTGGAAGTACTTTT 307
DB 241 AAAATAATCAAAATCAATGATACCTTACAAATTTGTTTAAAGTAAATCCTGGAAGTACTTTT 300
QY 308 TGGATCGAGAACCGATATCAACTGGTAATTTACTCAATTCATATTTCTCTGTCACTTTGTTTC 367
DB 301 TGGATCGAGAACCGATATCAACTGGTAATTTACTCAATTCATATTTCTCTGTCACTTTGTTTC 360
QY 368 AGTTTCTGGTATCTAACTTTTACACAGGGGGAGATTTTGTAGTTGATTAATAGATTTTG 427
DB 361 AGTTTATGTAATCTAACTTTTACACAGGGGGAGATTTTGTAGTTGATTAATAGATTTTG 420
QY 428 TATGGGAATAGTTGGCCCTTCTCAATGGGATGCATTTCTAGTACAAATTTGAACAAATTA 487
DB 421 TATGGGAATAGTTGGCCCTTCTCAATGGGATGCATTTCTAGTACAAATTTGAACAAATTA 480
QY 488 TTAATCAGAAGATAGCTGAATTTGCTAGGAATGCTCTATTTCTTAATTTTGAAGGATTAG 547
DB 481 TTAATCAGAAGATAGCTGAATTTGCTAGGAATGCTCTATTTCTTAATTTTGAAGGATTAG 540
QY 548 GAAACAAATTTCAATATATATGTGGAAGCAATTTAAAGAAATGGAAGAAATCCTTAATAATC 607
DB 541 GAAACAAATTTCAATATATATGTGGAAGCAATTTAAAGAAATGGAAGAAATCCTTAATAATC 600
QY 608 CAGGAACAGGACAGAGTAATGATCGCTTTTGTATATCTGTATGAGGCTACTTGAAGGG 667
DB 601 CAGGAACAGGACAGAGTAATGATCGCTTTTGTATATCTGTATGAGGCTACTTGAAGGG 660
QY 668 ACATCTCTCGTTTTCGAATTTTGAATTTGAGTACCCCTTTTATCCGTTTATGCTCAAG 727
DB 661 ACATCTCTCGTTTTCGAATTTTGAATTTGAGTACCCCTTTTATCCGTTTATGCTCAAG 720
QY 728 CGGCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTGGAGAAAGATGGGAT 787
DB 721 CGGCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTGGAGAAAGATGGGAT 780
QY 788 TGACACGATAAATGTCATGAAACTATATATAGACTAATTAAGGCATATTTGATGAATATG 847
DB 781 TGACACGATAAATGTCATGAAACTATATATAGACTAATTAAGGCATATTTGATGAATATG 840
QY 848 CTGATCAGTGTGCAAAATAGTATATCGGGATTAATAATTTACGAAATCTAGCTATC 907
DB 841 CTGATCAGTGTGCAAAATAGTATATCGGGATTAATAATTTACGAAATCTAGCTATC 900
QY 908 AAGATTGGATAACATATATCGATTACGAGAGACTTAACTATGACTGTATTAGATATCG 967
DB 901 AAGATTGGATAACATATATCGATTACGAGAGACTTAACTATGACTGTATTAGATATCG 960
QY 968 CCGCTTTTCTTCCAAACTATGACAAATAGAGATATCCAAATTCAGCCAGTTGGTCAACTAA 1027
DB 961 CCGCTTTTCTTCCAAACTATGACAAATAGAGATATCCAAATTCAGCCAGTTGGTCAACTAA 1020
QY 1028 CAAAGGAAGTTTATACGACCCCAATTAATTTTAAATCCACAGTTAGCTGTAGCTC 1087
DB 1021 CAAAGGAAGTTTATACGACCCCAATTAATTTTAAATCCACAGTTAGCTGTAGCTC 1080
QY 1088 AATTTACTCTTTTAACTGTTTGAAGAGCAGCGCAATTAAGAAATCCTCAATTTTGTGATA 1147
DB 1081 AATTTACTCTTTTAACTGTTTGAAGAGCAGCGCAATTAAGAAATCCTCAATTTTGTGATA 1140

QY 1148 TATTCGAATAATCTTCAAAATCTTTTACGGATTTGTTTGTAGTTGGACGCAATTTTATTTGGG 1207
DB 1141 TATTCGAATAATCTTCAAAATCTTTTACGGATTTGTTTGTAGTTGGACGCAATTTTATTTGGG 1200
QY 1208 GAGGACATCGAGTAATATCTAGCCTTATAGGAGGTGTAACATATACATCTCTCTATATATG 1267
DB 1201 GAGGACATCGAGTAATATCTAGCCTTATAGGAGGTGTAACATATACATCTCTCTATATATG 1260
QY 1268 GAAAGAGAGCGCAACCAAGGAGCCTCCAAGATCTCTTACTTTTAAATGGACCGGTATTTAGGA 1327
DB 1261 GAAAGAGAGCGCAACCAAGGAGCCTCCAAGATCTCTTACTTTTAAATGGACCGGTATTTAGGA 1320
QY 1328 CTTTATCAATTCCTTACTTTTACGATTTATACAGCAACCTTGGCAGCGCCACCAATTTAAT 1387
DB 1321 CTTTATCAATTCCTTACTTTTACGATTTATACAGCAACCTTGGCAGCGCCACCAATTTAAT 1380
QY 1388 TACGTGGTGTGAAGGAGTAGAATTTTCTACACCTTACAAATAGCTTTTACGTATCGAGGA 1447
DB 1381 TACGTGGTGTGAAGGAGTAGAATTTTCTACACCTTACAAATAGCTTTTACGTATCGAGGA 1440
QY 1448 GAGGTACCGTTTGAATTTTAACTGAATTTACCGCCTGAGGATTAATAGTGTGCCACCTCGCG 1507
DB 1441 GAGGTACCGTTTGAATTTTAACTGAATTTACCGCCTGAGGATTAATAGTGTGCCACCTCGCG 1500
QY 1508 AAGGATATAGTCAATCGTTTATGTCAAGCAACTTTTGTTCAAAGATCTCGAAACACCTTTT 1567
DB 1501 AAGGATATAGTCAATCGTTTATGTCAAGCAACTTTTGTTCAAAGATCTCGAAACACCTTTT 1560
QY 1568 TAAACAACTGGTGTAGTATTTTCTGGACGCATCTGTAGTGCACCTCTTACAAATACAAATG 1627
DB 1561 TAAACAACTGGTGTAGTATTTTCTGGACGCATCTGTAGTGCACCTCTTACAAATACAAATG 1620
QY 1628 ATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGAGATTTAGAGTTGGGGGGCACCT 1687
DB 1621 ATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGAGATTTAGAGTTGGGGGGCACCT 1680
QY 1688 CTGTCAATTAAGGACAGGATTTACAGAGGGGATATCTTTCGAAAGAAATACCTTTGGTG 1747
DB 1681 CTGTCAATTAAGGACAGGATTTACAGAGGGGATATCTTTCGAAAGAAATACCTTTGGTG 1740
QY 1748 ATTTTGTATCTCTACAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1807
DB 1741 ATTTTGTATCTCTACAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1800
QY 1808 TTCTGTCAGCTTCCAGTAGGAGTACAGCAGTTATAGTATTAACAGAGCGGATCCACAG 1867
DB 1801 TTCTGTCAGCTTCCAGTAGGAGTACAGCAGTTATAGTATTAACAGAGCGGATCCACAG 1860
QY 1868 GAGTGGGAGGCCAAAGTTAGTGTAGATATGCTTTCAGAAAACTATGAAAAATAGGGGAGA 1927
DB 1861 GAGTGGGAGGCCAAAGTTAGTGTAGATATGCTTTCAGAAAACTATGAAAAATAGGGGAGA 1920
QY 1928 ACTTAAATCTAGAACATTTAGATATACCGATTTTGTAGTAAATCTTTTCAATTTAGAGCTA 1987
DB 1921 ACTTAAATCTAGAACATTTAGATATACCGATTTTGTAGTAAATCTTTTCAATTTAGAGCTA 1980
QY 1988 ATCCAGATATATTTGGGATAAGTGAACCAACCTCTATTTTGTGTGCGAGTTCTTATAGTAGCG 2047
DB 1981 ATCCAGATATATTTGGGATAAGTGAACCAACCTCTATTTTGTGTGCGAGTTCTTATAGTAGCG 2040
QY 2048 TTGAATCTTATATAGATAAAATTTGAATTTTCTAGCAGATGCAACATTTTGAAGCAGAAAT 2107
DB 2041 TTGAATCTTATATAGATAAAATTTGAATTTTCTAGCAGATGCAACATTTTGAAGCAGAAAT 2100
QY 2108 CTGATTTAGAAAGAGCAAAAAGGGGTGAATGCGCTGTTTACTTTTCTTCCAAATCAAAATCG 2167
DB 2101 CTGATTTAGAAAGAGCAAAAAGGGGTGAATGCGCTGTTTACTTTTCTTCCAAATCAAAATCG 2160
QY 2168 GGTAAAAACCGATGTGACGATTTATCATATTTGATCAAGTATCCAAATTTAGTGGATGCTT 2227
DB 2161 GGTAAAAACCGATGTGACGATTTATCATATTTGATCAAGTATCCAAATTTAGTGGATGCTT 2220
QY 2228 TATCAGATGAATTTTGTCTCGATGAAAGAGCGAGAAATTTGTCGAGAGAAAGTCAAAATGCGA 2287

Db 841 GTAGCTCAATTACTTCTTTAAAGTTATGGAGAGCAGCGCAATTAGAAATCCTCATTTA 900
Qy 1141 TTTGATATATGTAATATCTTACAATCTTTACGGATTGGTTAGTGTGGAGCGCAATTTT 1200
Db 901 TTTGATATATGTAATATCTTACAATCTTTACGGATTGGTTAGTGTGGAGCGCAATTTT 960
Qy 1201 TATTGGGAGGACATCGAGTATATCTAGCTTTATAGGAGGTGGTAAATCATCTCTCT 1260
Db 961 TATTGGGAGGACATCGAGTATATCTAGCTTTATAGGAGGTGGTAAATCATCTCTCT 1020
Qy 1261 ATATATGGAAGAGAGCGGCAACAGGAGCCTTCAAGATCTTTTAAATGAGCGGTA 1320
Db 1021 ATATATGGAAGAGAGCGGCAACAGGAGCCTTCAAGATCTTTTAAATGAGCGGTA 1080
Qy 1321 TTTAGGACTTTATCAATCTCTTACTTTACGATTTATACAGCAACCTTGCAGCGCCACCAT 1380
Db 1081 TTTAGGACTTTATCAATCTCTTACTTTACGATTTATACAGCAACCTTGCAGCGCCACCA 1140
Qy 1381 TTTAATTTACGTTGGTGAAGAGTAGAATTTTCTACACCTTACAAATAGCTTTAGTAT 1440
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Qy 1441 GCAGGAAGAGGTACGGTTGATCTTTAACTTGAATACCGCTGAGGATAATAGTGCCA 1500
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Qy 1501 CCTCGGAAGGATATAGTATCATCGTTTATGTCAGCAACTTTTGTTCAAAGATCTGGAACA 1560
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Qy 1561 CCTTTTAACTCGTGTAGTATTTTCTTGGAAGCATCGTAGTGCAACTCTTTCAAAAT 1620
Db 1321 CCTTTTAACTCGTGTAGTATTTTCTTGGAAGCATCGTAGTGCAACTCTTTCAAAAT 1380
Qy 1621 ACAATTTGATCCAGAGAGATTAATCAATACCTTTTGTGAAAGGATTTAGTGTGGGG 1680
Db 1381 ACAATTTGATCCAGAGAGATTAATCAATACCTTTTGTGAAAGGATTTAGTGTGGGG 1440
Qy 1681 GGCACCTCTGTCTATACAGGACAGGATTTACAGGAGGGGATATCTTCGAAAGAAATACC 1740
Db 1441 GGCACCTCTGTCTATACAGGACAGGATTTACAGGAGGGGATATCTTCGAAAGAAATACC 1500
Qy 1741 TTTGGTGAATTTGTATCTCTACAGTCAATATTAATTCACCAATTTACCAAGATACCGT 1800
Db 1501 TTTGGTGAATTTGTATCTCTACAGTCAATATTAATTCACCAATTTACCAAGATACCGT 1560
Qy 1801 TTAAGATTTGTTACGCTTCCAGTAGGAGTGAGGATTTAGTATTAACAGAGCGCA 1860
Db 1561 TTAAGATTTGTTACGCTTCCAGTAGGAGTGAGGATTTAGTATTAACAGAGCGCA 1620
Qy 1861 TCCACAGGAGTGGGAGGCGCAAGTTAGTATGATATGCTCTTCAGAAACTATGGAATA 1920
Db 1621 TCCACAGGAGTGGGAGGCGCAAGTTAGTATGATATGCTCTTCAGAAACTATGGAATA 1680
Qy 1921 GGGGAGAACTTAACATCTAGAACATTTAGATATACGATTTTGTAGTATCTTTTCAAT 1980
Db 1681 GGGGAGAACTTAACATCTAGAACATTTAGATATACGATTTTGTAGTATCTTTTCAAT 1740
Qy 1981 AGAGCTAATCCAGATATTAATGGAATAGTGAACCTCTATTTGGTGACGTTCTATT 2040
Db 1741 AGAGCTAATCCAGATATTAATGGAATAGTGAACCTCTATTTGGTGACGTTCTATT 1800
Qy 2041 AGTAGCGTTGAATCTTTATATAGATAAAATTTGAAATTTTCTAGCAGATGCAACATTTGAA 2100
Db 1801 AGTAGCGTTGAATCTTTATATAGATAAAATTTGAAATTTTCTAGCAGATGCAACATTTGAA 1860
Qy 2101 CGAGAACTTGATTTGAAAGAGACAAAAGCGGTAATGCGCTGTTTACTTTTCCAAT 2160
Db 1861 CGAGAACTTGATTTGAAAGAGACAAAAGCGGTAATGCGCTGTTTACTTTTCCAAT 1920
Qy 2161 CAAATCGGTTAAAAACCGATGTGACGGAATATCATATTTGATCAAGTATCCAATTTAGTG 2220
Db 1921 CAAATCGGTTAAAAACCGATGTGACGGAATATCATATTTGATCAAGTATCCAATTTAGTG 1980

Qy 2221 GATTGTTTATCAGATGAATTTTGTCTGGATGAAAAAGCAGAAATTTGTCGAGAAAGTCAAA 2280
Db 1981 GATTGTTTATCAGATGAATTTTGTCTGGATGAAAAAGCAGAAATTTGTCGAGAAAGTCAAA 2040
Qy 2281 CATGGAAGCGACTCAGTGAATGAGCGGAATTTTACTTCAAGATCCAAAATTTCAAGAGGATC 2340
Db 2041 CATGGAAGCGACTCAGTGAATGAGCGGAATTTTACTTCAAGATCCAAAATTTCAAGAGGATC 2100
Qy 2341 AATAGACAACACAGACCGCTGGCTGGAGAGGAAGTACAGATATTTACCATCCAGGAGAGAT 2400
Db 2101 AATAGACAACACAGACCGCTGGCTGGAGAGGAAGTACAGATATTTACCATCCAGGAGAGAT 2160
Qy 2401 GACGTATTTCAAGAGAAATTTACGTACACTACCGGTACCGTTTGTAGTGTCTATCCAAAG 2460
Db 2161 GACGTATTTCAAGAGAAATTTACGTACACTACCGGTACCGTTTGTAGTGTCTATCCAAAG 2220
Qy 2461 TATTATATCAGAAAAATAGATGAGTCAAAATTTAAAAGCTTATACCGTTTATGAATTAAGA 2520
Db 2221 TATTATATCAGAAAAATAGATGAGTCAAAATTTAAAAGCTTATACCGTTTATGAATTAAGA 2280
Qy 2521 GGGTATATCGAAGATAGTCAAGACTTTAGAAATCTTATTTGATCGCTTACAAATGCAAAACAC 2580
Db 2281 GGGTATATCGAAGATAGTCAAGACTTTAGAAATCTTATTTGATCGCTTACAAATGCAAAACAC 2340
Qy 2581 GAAATAGTAAATGTGCCAGGACCGGTTCTTTATGCGCGCTTTTACAGCCAAAGTCCAATC 2640
Db 2341 GAAATAGTAAATGTGCCAGGACCGGTTCTTTATGCGCGCTTTTACAGCCAAAGTCCAATC 2400
Qy 2641 GGAAGTGTGGAAGAACCGAATCGATGCGCGCCACACTTTGAATGAATCTCTGATCTAGAT 2700
Db 2401 GGAAGTGTGGAAGAACCGAATCGATGCGCGCCACACTTTGAATGAATCTCTGATCTAGAT 2460
Qy 2701 TGTTCTCTGACG 2711
Db 2461 TGTTCTCTGACG 2471

RESULT 6

US-09-001-982-1
; Sequence 1, Application US/09001982
; Patent No. 6204246
; GENERAL INFORMATION:
; APPLICANT: Bosch, Hendrick J.
; APPLICANT: Stiekema, Willem J.
; TITLE OF INVENTION: Hybrid Toxin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6204246artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/001.982
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/602,737
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: *Bacillus thuringiensis*
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3567
US-09-001-982-1

Query Match 89.7%; Score 2431; DB 3; Length 3567;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2446; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy	241	ATGAGGAAATTAATCAAAATCAATGATACCTTACAAATGTTTAAAGTAATCTGAAGAA	300
Db	1	ATGAGGAAATTAATCAAAATCAATGATACCTTACAAATGTTTAAAGTAATCTGAAGAA	60
Qy	301	GTACTTTGATGAGAACGGATCACTGATGATTAATCAATGATTAATTTCTCTGCA	360
Db	61	GTACTTTGATGAGAACGGATCACTGATGATTAATCAATGATTAATTTCTCTGCA	120
Qy	361	CTTGTTCAGTTTCTGATCTAACTTTGACACGGGGAGGATTTTGTGATTAATA	420
Db	121	CTTGTTCAGTTTCTGATCTAACTTTGACACGGGGAGGATTTTGTGATTAATA	180
Qy	421	GATTTTGTGAGGAAATAGTTGGCCCTTCAATGGGATGCAATTTCTGATTAATA	480
Db	181	GATTTTGTGAGGAAATAGTTGGCCCTTCAATGGGATGCAATTTCTGATTAATA	240
Qy	481	CAATTAATTAATGAAGAATAGCTGAATTTGCTAGAAATGCTGATTTTGAAGA	540
Db	241	CAATTAATTAATGAAGAATAGCTGAATTTGCTAGAAATGCTGATTTTGAAGA	300
Qy	541	GGATTTAGAAACAATTTCAATATATATGAGAAAGCAATTAAGAAATGGGAGAGATCT	600
Db	301	GGATTTAGAAACAATTTCAATATATATGAGAAAGCAATTAAGAAATGGGAGAGATCT	360
Qy	601	AATAATCCAGCAACCCAGGACAGAGTAATGATCGCTTTTCGTATATGATGGGCTACTT	660
Db	361	AATAATCCAGCAACCCAGGACAGAGTAATGATCGCTTTTCGTATATGATGGGCTACTT	420
Qy	661	GAAAGGACATTCCTTCGTTTCGAATTTCTGGAATTTGAAAGTACCCCTTTTATCCGTTAT	720
Db	421	GAAAGGACATTCCTTCGTTTCGAATTTCTGGAATTTGAAAGTACCCCTTTTATCCGTTAT	480
Qy	721	GCTCAAGCGCCCAATCTGCATCTAGCTATATTAAGAGATCTGTAAATTTTGGAGAAAGA	780
Db	481	GCTCAAGCGCCCAATCTGCATCTAGCTATATTAAGAGATCTGTAAATTTTGGAGAAAGA	540
Qy	781	TTGGGATTCGACGATTAATGTCATGAATATTAATAGACTAATTAAGACTAATTTGAT	840
Db	541	TTGGGATTCGACGATTAATGTCATGAATATTAATAGACTAATTAAGACTAATTTGAT	600
Qy	841	GATATCTGATCTGATCTGATATGATATGATATGATATGATATGATATGATATGAT	900
Db	601	GATATCTGATCTGATCTGATATGATATGATATGATATGATATGATATGATATGAT	660
Qy	901	ACGATCAAGATTTGATTAATCAATATGATATGATATGATATGATATGATATGAT	960
Db	661	ACGATCAAGATTTGATTAATCAATATGATATGATATGATATGATATGATATGAT	720
Qy	961	GATATCGCGCTTTCTTCCAACTATGATATGATATGATATGATATGATATGAT	1020
Db	721	GATATCGCGCTTTCTTCCAACTATGATATGATATGATATGATATGATATGAT	780
Qy	1021	CAACTAAAGGGAAGTTTATACGGACCCCAATTAATTAATTTTAAATCCACAGTTACAGTCT	1080

8,100

Db	781	CAACTAAAGGGAAGTTTATACGGACCCCAATTAATTAATTTTAAATCCACAGTTACAGTCT	840
Qy	1081	GTAGCTCAATTTACCTACTACTTTTAAAGTTATGAGAGAGCGGCAATTAGAATCTCATTTA	1140
Db	841	GTAGCTCAATTTACCTACTACTTTTAAAGTTATGAGAGAGCGGCAATTAGAATCTCATTTA	900
Qy	1141	TTTGATATATTGAATAATCTTCAATCTTTACGATTTGGTTTATGTTTGGACGCAATTTT	1200
Db	901	TTTGATATATTGAATAATCTTCAATCTTTACGATTTGGTTTATGTTTGGACGCAATTTT	960
Qy	1201	TATTGGGAGGACATCGAGTAATATCTAGCCTTTATAGGAGTGGTAAATATAATCTCTCT	1260
Db	961	TATTGGGAGGACATCGAGTAATATCTAGCCTTTATAGGAGTGGTAAATATAATCTCTCT	1020
Qy	1261	ATATATGAGAGAGGCGGAACAGGAGCCTTCAAGATCTTCTTATCTTTTAAATGACCGGTA	1320
Db	1021	ATATATGAGAGAGGCGGAACAGGAGCCTTCAAGATCTTCTTATCTTTTAAATGACCGGTA	1080
Qy	1321	TTTAGACCTTTTCAATCTTCTACTTTTACGATTTTACGAACTTTCAGAGCCTTGGCCAGGCCACCA	1380
Db	1081	TTTAGACCTTTTCAATCTTCTACTTTTACGATTTTACGAACTTTCAGAGCCTTGGCCAGGCCACCA	1140
Qy	1381	TTTAATTTTACGTTGTTGAGAGTGAATTTTCTACACCTTACAAATAGCTTTTACGTAT	1440
Db	1141	TTTAATTTTACGTTGTTGAGAGTGAATTTTCTACACCTTACAAATAGCTTTTACGTAT	1200
Qy	1441	GCAGGAGAGGTACGGTTGATTTCTTAACTGAATTTACCGCTGAGGATAATAGTTGGCCA	1500
Db	1201	GCAGGAGAGGTACGGTTGATTTCTTAACTGAATTTACCGCTGAGGATAATAGTTGGCCA	1260
Qy	1501	CCTCGGAGAGGATAGTCAATGTTTATGTCATGCACTTTTGTCAAGATCTTGAAGA	1560
Db	1261	CCTCGGAGAGGATAGTCAATGTTTATGTCATGCACTTTTGTCAAGATCTTGAAGA	1320
Qy	1561	CTTTTAAACAACTGGTGTAGTATTTCTTGAAGCATGTCGACCTTCTTCAAAAT	1620
Db	1321	CTTTTAAACAACTGGTGTAGTATTTCTTGAAGCATGTCGACCTTCTTCAAAAT	1380
Qy	1621	ACAAATGATCCAGAGAGAAATTAATCAATTAATGTAAGGATTTAGTTTGGGG	1680
Db	1381	ACAAATGATCCAGAGAGAAATTAATCAATTAATGTAAGGATTTAGTTTGGGG	1440
Qy	1681	GGCACTCTGTCTATTTACAGGACCAAGATTTACAGAGGGGATATCTTTCGAAGAATACC	1740
Db	1441	GGCACTCTGTCTATTTACAGGACCAAGATTTACAGAGGGGATATCTTTCGAAGAATACC	1500
Qy	1741	TTTGTGATTTTGTATCTCTACAAAGTCAATATTAATTCACAAATACC	1800
Db	1501	TTTGTGATTTTGTATCTCTACAAAGTCAATATTAATTCACAAATACC	1560
Qy	1801	TTAAGATTTGTTTGTATCTCTACAAAGTCAATATTAATTCACAAAGTCAATACC	1860
Db	1561	TTAAGATTTGTTTGTATCTCTACAAAGTCAATATTAATTCACAAAGTCAATACC	1620
Qy	1861	TCCACAGGTTGGGAGGCGCAAGTTAGTGTAGATATGCTCTTTCAGAAAATATGAAATA	1920
Db	1621	TCCACAGGTTGGGAGGCGCAAGTTAGTGTAGATATGCTCTTTCAGAAAATATGAAATA	1680
Qy	1921	GGGAGGAACTTACATCTAGAACATTTAGATATACCGATTTTATGATATCTTTTCAATT	1980
Db	1681	GGGAGGAACTTACATCTAGAACATTTAGATATACCGATTTTATGATATCTTTTCAATT	1740
Qy	1981	AGAGCTAATCCAGATTAATTTGGGTAAGTGAACACCTCTATTTTGGTGGAGGTTCTATT	2040
Db	1741	AGAGCTAATCCAGATTAATTTGGGTAAGTGAACACCTCTATTTTGGTGGAGGTTCTATT	1800
Qy	2041	AGTACGGTGAACCTTTATATAGATTAATTTGAAATTTTCTAGCAGATGCAATTTGAA	2100
Db	1801	AGTACGGTGAACCTTTATATAGATTAATTTGAAATTTTCTAGCAGATGCAATTTGAA	1860
Qy	2101	GCAGAACTCTGATTTAGAAAGGAGCACAAGGCGGTGAATGCCCTTTTCTTCTTCAAT	2160

Db 1861 GCAGAACTCTGATTAGAAAGACACAAAAGCGGTGAATGCCCTGTTTACTTCTTCCAAAT 1920
 QY 2161 CAAATCGGGTTAAAAACCGATGTGACGGATTAATCATATTGATCAAGTATCCAAATTTAGTG 2220
 Db 1921 CAAATCGGGTTAAAAACCGATGTGACGGATTAATCATATTGATCAAGTATCCAAATTTAGTG 1980
 QY 2221 GATTGTTTATCAGATGAATTTTGTCTGGATGAAAAGCGGAAATGTCCGAGAAAGTCAAA 2280
 Db 1981 GATTGTTTATCAGATGAATTTTGTCTGGATGAAAAGCGGAAATGTCCGAGAAAGTCAAA 2040
 QY 2281 CATGCGAAGCGACTCAGTGATGATGCGGAATTTACTTTCAAGATCCAAACTTTACAGGGATC 2340
 Db 2041 CATGCGAAGCGACTCAGTGATGATGCGGAATTTACTTTCAAGATCCAAACTTTACAGGGATC 2100
 QY 2341 AATAGACAACACGACCGTGGCTGGAGAGGAAGTACAGATTAATACCAATCCAAAGGAGAT 2400
 Db 2101 AATAGACAACACGACCGTGGCTGGAGAGGAAGTACAGATTAATACCAATCCAAAGGAGAT 2160
 QY 2401 GAGTATTCAAAGAGAAATACGTACACTACCGGGTACCGTTGATGAGTGCTATCCAAG 2460
 Db 2161 GAGTATTCAAAGAGAAATACGTACACTACCGGGTACCGTTGATGAGTGCTATCCAAG 2220
 QY 2461 TATTTATATCAGAAAATAGATGATCGAAATTAAGAGCTTATACCCGTTATGAATTAAGA 2520
 Db 2221 TATTTATATCAGAAAATAGATGATCGAAATTAAGAGCTTATACCCGTTATGAATTAAGA 2280
 QY 2521 GGTATATCAAGATAGTCAAGACTTAGAAATCTATTTGATCGGTACCAATGCAAAACAC 2580
 Db 2281 GGTATATCAAGATAGTCAAGACTTAGAAATCTATTTGATCGGTACCAATGCAAAACAC 2340
 QY 2581 GAAATAGTAAATGTCGACGACGGGTTCTTATGCGCGTTTACGCCCAAAAGTCCAATC 2640
 Db 2341 GAAATAGTAAATGTCGACGACGGGTTCTTATGCGCGTTTACGCCCAAAAGTCCAATC 2400
 QY 2641 GGAAGTGTGGAACCGGAATCGATCGCGCACACCTTGAATGGAATCCTGATCTAGAT 2700
 Db 2401 GGAAGTGTGGAACCGGAATCGATCGCGCACACCTTGAATGGAATCCTGATCTAGAT 2460
 QY 2701 TGTCTCTGCAG 2711
 Db 2461 TGTCTCTGCAG 2471

RESULT 7

US-07-828-788A-15
 ; Sequence 15, Application US/07828788A
 ; Patent No. 5273746
 ; GENERAL INFORMATION:
 ; APPLICANT: PAYNE, JEWEL M.
 ; APPLICANT: HICKLE, LESLIE A.
 ; TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
 ; TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DAVID R. SALIWANCHIK
 ; STREET: 2421 N.W. 41st STREET, SUITE A-1
 ; CITY: GAINESVILLE
 ; STATE: FL
 ; COUNTRY: USA
 ; ZIP: 32606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/828,788A
 ; FILING DATE: 19920129
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SALIWANCHIK, DAVID R.
 ; REGISTRATION NUMBER: 31,794
 ; REFERENCE/DOCKET NUMBER: MA75

TELECOMMUNICATION INFORMATION:

; TELEPHONE: 904-375-8100
 ; TELEFAX: 904-372-5800
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3567 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: BACILLUS THURINGIENSIS
 ; STRAIN: AIZAWAI
 ; INDIVIDUAL ISOLATE: PS811
 ; IMMEDIATE SOURCE:
 ; LIBRARY: LAMBDA GEM (TM) - 11 LIBRARY OF AUGUST SICK
 ; CLONE: 811B2
 ; US-07-828-788A-15

Query Match 89.6%; Score 2429.4; DB 1; Length 3567;

Best Local Similarity 98.9%; Pred. No. 0; Mismatches 26; Indels 0; Gaps 0;

Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 241 ATGGAGGAAAATAATCAAAATCAATGCATACCTTACAAATGTTTAAAGTAATCTCGAAGAA 300
 Db 1 ATGGAGGAAAATAATCAAAATCAATGCATACCTTACAAATGTTTAAAGTAATCTCGAAGAA 60
 QY 301 GTACTTTGGATGGAGAACGGATATCAACTGGTAATTAATCAATTTGATGATATTTCTGTCA 360
 Db 61 GTACTTTGGATGGAGAACGGATATCAACTGGTAATTAATCAATTTGATGATATTTCTGTCA 120
 QY 361 CTGTGTTGAGTTTCTGGTATCTAACTTTGTACAGGGGGAGGATTTTGTAGTTCGATTAATA 420
 Db 121 CTGTGTTGAGTTTCTGGTATCTAACTTTGTACAGGGGGAGGATTTTGTAGTTCGATTAATA 180
 QY 421 GATTTTGTATGGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTTGAA 480
 Db 181 GATTTTGTATGGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTTGAA 240
 QY 481 CAATTAATTAAGAAAGAAATAGCTGAATTTGCTAGGAATGCTGCTATTTGCTAATTTAGAA 540
 Db 241 CAAATTAATTAAGAAAGAAATAGCTGAATTTGCTAGGAATGCTGCTATTTGCTAATTTAGAA 300
 QY 541 GGATTTAGGAACAATTTCAATATATATGTGGAAGCATTTAAAGAAATGGGAAGATCCCT 600
 Db 301 GGATTTAGGAACAATTTCAATATATATGTGGAAGCATTTAAAGAAATGGGAAGATCCCT 360
 QY 601 AATAATCCAGCAACCCAGGACAGAGTAATTTGATCGCTTTTCGTATATCTTGTATGCTGCTACTT 660
 Db 361 AATAATCCAGCAACCCAGGACAGAGTAATTTGATCGCTTTTCGTATATCTTGTATGCTGCTACTT 420
 QY 661 GAAAGGGAATTTCTTCTGTTTCGAATTTCTGGAATTTGAAGTACCCCTTTTATCCGTTTAT 720
 Db 421 GAAAGGGAATTTCTTCTGTTTCGAATTTCTGGAATTTGAAGTACCCCTTTTATCCGTTTAT 480
 QY 721 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTGTGAGAGAGA 780
 Db 481 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTGTGAGAGAGA 540
 QY 781 TTGGGATTTGACAAACGATAAATGTCAATGAAACTATAATAGACTAATTTAGGCAATTTGAT 840
 Db 541 TTGGGATTTGACAAACGATAAATGTCAATGAAACTATAATAGACTAATTTAGGCAATTTGAT 600
 QY 841 GAATATGCTGATCACTGTGCAAAATACGTATTAATCGGGGATTAATAATTTACCGAAATCT 900
 Db 601 GAATATGCTGATCACTGTGCAAAATACGTATTAATCGGGGATTAATAATTTACCGAAATCT 660
 QY 901 ACGTATCAAGATTGGATTAACATATATTCGATTAACCGAGAGACTTAACTTGAATCTGATTA 960
 Db 661 ACGTATCAAGATTGGATTAACATATATTCGATTAACCGAGAGACTTAACTTGAATCTGATTA 720

1801 AGTAGCGGTGAACCTTTATATAGATAAAATTTAGTATGATGCAATTTGAA 1860
2101 GCAGAACTCTGATTTAGAAAGAGACAAAAGCGGTGAATGCCCTTTTCTTCCAAAT 2160
1861 GCAGAACTCTGATTTAGAAAGAGACAAAAGCGGTGAATGCCCTTTTCTTCCAAAT 1920
2161 CAATCCGGTTTAAAACCGATGTCACGATTTATCATATTTGATCAAGTATCAATTTAGTG 2220
1921 CAATCCGGTTTAAAACCGATGTCACGATTTATCATATTTGATCAAGTATCAATTTAGTG 1980
2221 GATTTGTTATCAGATCAATTTTGTCTGATGAAAACCGAGAAATTTGTCGAGAAAGTCAAA 2280
1981 GATTTGTTATCAGATCAATTTTGTCTGATGAAAACCGAGAAATTTGTCGAGAAAGTCAAA 2040
2281 CATGCGAAGCGCTCAGTCTGATGAGCGGAATTTTACTTCAAGATCCAAACTTCAGAGGATC 2340
2041 CATGCGAAGCGCTCAGTCTGATGAGCGGAATTTTACTTCAAGATCCAAACTTCAGAGGATC 2100
2341 ATAGACAAACGACCGTGGCTGAGAGGAGTACAGATATTACCATCAAGAGGAGAT 2400
2101 AATAGACAAACGACCGTGGCTGAGAGGAGTACAGATATTACCATCAAGAGGAGAT 2160
2401 GAGTATTTAAAGAAATTTACGTCACCTACCGGTACCGTTGATGAGTGTCTTCAACG 2460
2161 GAGTATTTAAAGAAATTTACGTCACCTACCGGTACCGTTGATGAGTGTCTTCAACG 2220
2461 TATTTATATCAGAAATTTAGATGAGTCAAGATTTAAAGCTTATACCGTTTGAATTAAGA 2520
2221 TATTTATATCAGAAATTTAGATGAGTCAAGATTTAAAGCTTATACCGTTTGAATTAAGA 2280
2521 GGGTATATCGAAGATAGTCAAGATTTAGAAATTTATTTGATCGGTACAAATCGAAGAC 2580
2281 GGGTATATCGAAGATAGTCAAGATTTAGAAATTTATTTGATCGGTACAAATCGAAGAC 2340
2581 GAAATAGTAAATTTGTCAGACGACGGTTCTTTATGGCGCTTTTCAAGCCAAAGTCCAAATC 2640
2341 GAAATAGTAAATTTGTCAGACGACGGTTCTTTATGGCGCTTTTCAAGCCAAAGTCCAAATC 2400
2641 GGAAAGTGGGAGAACCGAATTCGATCGCGCCACACCTTGAATGGAATCTGATCTAGAT 2700
2401 GGAAAGTGGGAGAACCGAATTCGATCGCGCCACACCTTGAATGGAATCTGATCTAGAT 2460
2701 TGTTCTCTGAG 2711
2461 TGTTCTCTGAG 2471

RESULT 8
US-08-356-034-5
; Sequence 5, Application US/08356034
; Patent No. 5691308
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; TITLE OF INVENTION: No. 5691308 Bacillus thuringiensis Isolate
; TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding
; TITLE OF INVENTION: No. 5691308 Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,034

;; FILING DATE: 435
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/210,110
;; FILING DATE: 07/865,168
;; APPLICATION NUMBER: 07/865,168
;; FILING DATE: 09-APR-92
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/451,261
;; FILING DATE: 14-DEC-89
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/371,955
;; FILING DATE: 27-JUN-89
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Saliwanchik, Roman
;; REGISTRATION NUMBER: 21,023
;; REFERENCE/DOCKET NUMBER: MR43.C1.D1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (904)375-8100
;; TELEFAX: (904)372-5800
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3567 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: BACILLUS THURINGIENSIS
;; STRAIN: AIZAWAI
;; INDIVIDUAL ISOLATE: PS811
;; IMMEDIATE SOURCE:
;; LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
;; CLONE: 811B2
US-08-356-034-5

Query Match 89.6%; Score 2429.4; DB 1; Length 3567;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY	241	ATGAGGAAATATCAAAATCAATGATACATCACTTCAATTTGTTAAAGTAACTCTGAAGAA	300
DB	1	ATGAGGAAATATCAAAATCAATGATACATCACTTCAATTTGTTAAAGTAACTCTGAAGAA	60
QY	301	GTACTTTTGGATGGAGAACGGATATCAACTGGGPAATTAATCTCAATTCATATTTCTCTGTCA	360
DB	61	GTACTTTTGGATGGAGAACGGATATCAACTGGGPAATTAATCTCAATTCATATTTCTCTGTCA	120
QY	361	CTTGTTTCAGTTCTGCTATCTAATTTGTTACAGGGGGAGGATTTTAGTGGATTAATA	420
DB	121	CTTGTTTCAGTTCTGCTATCTAATTTGTTACAGGGGGAGGATTTTAGTGGATTAATA	180
QY	421	GATTTTGTATGGGAATAGTTGGCCCTTCTCAATGGGATGTCATTTCTAGTACAAATTTGAA	480
DB	181	GATTTTGTATGGGAATAGTTGGCCCTTCTCAATGGGATGTCATTTCTAGTACAAATTTGAA	240
QY	481	CAATTAATTAAGAAAGATAGCTGAATTTGTTAGGAATGCTGCTATTTGCTAATTTAGAA	540
DB	241	CAATTAATTAAGAAAGATAGCTGAATTTGTTAGGAATGCTGCTATTTGCTAATTTAGAA	300
QY	541	GGATTAGGAACAATTTCAATATATATGTGGAGCAATTAAGAAATGGGAAGAGATCCT	600
DB	301	GGATTAGGAACAATTTCAATATATATGTGGAGCAATTTAAAGAAATGGGAAGAGATCCT	360
QY	601	AATAATCCAGCAACAGGACAGAGTAAATTTGATCGCTTTGCTATCTGATGGGCTACTT	660
DB	361	AATAATCCAGCAACAGGACAGAGTAAATTTGATCGCTTTGCTATCTGATGGGCTACTT	420
QY	661	GAAAGGACATTCCTTCGTTTTCGAATTTCTGGATTTGAAAGTACCCCTTTTATCCGTTTAT	720

DB	421	GAAAGGACATTCCTTCGTTTTCGAATTTCTGGATTTGAAAGTACCCCTTTTATCCGTTTAT	480
QY	721	GCTCAAGCGGCAATCTGCATCTAGCTATATTAAGAGATTCTGTAATTTTGGAGAAAGA	780
DB	481	GCTCAAGCGGCAATCTGCATCTAGCTATATTAAGAGATTCTGTAATTTTGGAGAAAGA	540
QY	781	TTGGGATTGACAAACGATAAATGTCAATGAAACTATAATAGACTAATTAGGCATATTGAT	840
DB	541	TGGGGATTGACAAACGATAAATGTCAATGAAACTATAATAGACTAATTAGGCATATTGAT	600
QY	841	GAATATGCTGATCACTGTGCAAAATAGCTAATCGGGGATTTAAATATTACCGAAATCT	900
DB	601	GAATATGCTGATCACTGTGCAAAATAGCTAATCGGGGATTTAAATATTACCGAAATCT	660
QY	901	ACGTATCAAGATTGGGTAACATATATCGATTACGGAGAGACTTAACTTTGACTGATTTA	960
DB	661	ACGTATCAAGATTGGGTAACATATATCGATTACGGAGAGACTTAACTTTGACTGATTTA	720
QY	961	GATATCGCGCTTTCTTTCCAAACTATGACAAATAGGAGATATCCAAATTCAGCCAGTTGGT	1020
DB	721	GATATCGCGCTTTCTTTCCAAACTATGACAAATAGGAGATATCCAAATTCAGCCAGTTGGT	780
QY	1021	CAACTAAAGGGAAGTTTATACGGACCCATTAATTAATTTTAATCCACAGTTACAGTCT	1080
DB	781	CAACTAAAGGGAAGTTTATACGGACCCATTAATTAATTTTAATCCACAGTTACAGTCT	840
QY	1081	GTAGCTCAATTAACCTTTTAACTGATGGAGCGCGCAATTAAGAAATCTCAATTTA	1140
DB	841	GTAGCTCAATTAACCTTTTAACTGATGGAGCGCGCAATTAAGAAATCTCAATTTA	900
QY	1141	TTTGATATATCAATAATCTTACAATCTTTACGGATTGTTAGTGTGGAGCAATTTT	1200
DB	901	TTTGATATATCAATAATCTTACAATCTTTACGGATTGTTAGTGTGGAGCAATTTT	960
QY	1201	TATTTGGGAGGACATCGAGTAATATCTAGCTTTATAGGAGGTGGTAAATACATCTCT	1260
DB	961	TATTTGGGAGGACATCGAGTAATATCTAGCTTTATAGGAGGTGGTAAATACATCTCT	1020
QY	1261	ATATATGGAAGAGGCGAACAGGAGCTTCAAGATCTTTTACTTTTAAATGGACGGTA	1320
DB	1021	ATATATGGAAGAGGCGAACAGGAGCTTCAAGATCTTTTACTTTTAAATGGACGGTA	1080
QY	1321	TTTAGGACTTTTCAATCTCTTACGATTTTACGAACTTACAGCACTTCCAGCGCCACCAT	1380
DB	1081	TTTAGGACTTTTCAATCTCTTACGATTTTACGAACTTACAGCACTTCCAGCGCCACCAT	1140
QY	1381	TTTAATTTACGTTGGTGAAGAGTAGAATTTTCTACACCTTACAAATAGCTTTACGTAT	1440
DB	1141	TTTAATTTACGTTGGTGAAGAGTAGAATTTTCTACACCTTACAAATAGCTTTACGTAT	1200
QY	1441	CGAGGAAGGTTACGTTGATTTTAACTGAAATTTACCGCTTGAAGATTAATAGTGGCCA	1500
DB	1201	CGAGGAAGGTTACGTTGATTTTAACTGAAATTTACCGCTTGAAGATTAATAGTGGCCA	1260
QY	1501	CCTCGCAAGGATATAGTATCATCGTTTATGTCAATGAACTTTTGTTCGAAAGATCTGGAACA	1560
DB	1261	CCTCGCAAGGATATAGTATCATCGTTTATGTCAATGAACTTTTGTTCGAAAGATCTGGAACA	1320
QY	1561	CTTTTTTAACTGTTGTTAGTATTTTCTTGGACGCAATCGTAGTGCAACTCTTTACAAAT	1620
DB	1321	CTTTTTTAACTGTTGTTAGTATTTTCTTGGACGCAATCGTAGTGCAACTCTTTACAAAT	1380
QY	1621	ACAAATGATCCAGAGAGATTAATCAATACCTTTAGTGAAGAGATTAAGTGGGGG	1680
DB	1381	ACAAATGATCCAGAGAGATTAATCAATACCTTTAGTGAAGAGATTAAGTGGGGG	1440
QY	1681	GGCACTCTGCTATTACAGGACAGATTTTACAGAGGGGATATCTCTCGAAGAAATACC	1740
DB	1441	GGCACTCTGCTATTACAGGACAGATTTTACAGAGGGGATATCTCTCGAAGAAATACC	1500
QY	1741	TTTGGTGAATTTTGTATCTCTCAAGTCAATATTAATTCACCAATTTACCCAAAGATACCGT	1800

GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Gilmer, Amy Jelen
APPLICANT: Mettels, Anne-Marie Light
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
TITLE OF INVENTION: LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,071
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA: US 08/757,536
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3567
US-08-980-071-11

Query Match 89.6%; Score 2429.4; DB 2; Length 3567;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 241 ATCGAGGAATATCAAAATCAATGATACCTTACAAATGTTTAAAGTAATCTCTGAAGAA 300
DB 1 ATGGAGAAATATCAAAATCAATGATACCTTACAAATGTTTAAAGTAATCTCTGAAGAA 60
QY 301 GTACTTTGGATGGAGACGGATATCACTGTAATTAATCAATGATATTTCTCTGTCA 360
DB 61 GTACTTTGGATGGAGACGGATATCACTGTAATTAATCAATGATATTTCTCTGTCA 120
QY 361 CTGTTTCAGTTTCTGGTATCTAATCTTTGACCGGGGAGATTTTAAAGTAAATTAATA 420
DB 121 CTGTTTCAGTTTCTGGTATCTAATCTTTGACCGGGGAGATTTTAAAGTAAATTAATA 180
QY 421 GATTTGTATGGGAATAGTTGGCCCTTCTCAATGGATGCAATTTCTAGTCAAAATGAA 480
DB 181 GATTTGTATGGGAATAGTTGGCCCTTCTCAATGGATGCAATTTCTAGTCAAAATGAA 240
QY 481 CAATTAATTAAGAAAGATAGCTGAATTTGCTAGGAATGCTGCTAATTTAGAAATTAAGA 540
DB 241 CAATTAATTAAGAAAGATAGCTGAATTTGCTAGGAATGCTGCTAATTTAGAAATTAAGA 300
QY 541 GATTTAGGAACCAATTTCAATATATATATGTTGAAGCAATTTAAAGATGGGAAGATCCT 600
DB 301 GATTTAGGAACCAATTTCAATATATATATGTTGAAGCAATTTAAAGATGGGAAGATCCT 360
QY 601 AATAATCCAGCAACACGAGGAGTAATTTGATCGCTTTCGTATACCTTGATGGGTACTT 660

361 CATATCCAGCAACACGAGGAGTAATTTGATCGCTTTCGTATACCTTGATGGGTACTT 420
QY 661 GAAAGGACATCTCTTTCGTTTCGAATTTCTGGAATTTGAAGTACCCCTTTTATCCGTTTAT 720
DB 421 GAAAGGACATCTCTTTCGTTTCGAATTTCTGGAATTTGAAGTACCCCTTTTATCCGTTTAT 480
QY 721 GCTCAAGCGGCAATCTGCATCTAGCTATATAAAGAGATTTCTGTAATTTTGGAGAAAGA 780
DB 481 GCTCAAGCGGCAATCTGCATCTAGCTATATAAAGAGATTTCTGTAATTTTGGAGAAAGA 540
QY 781 TTGGGATTGACACGATAAATCTCAATGAAATCTATAAAGAGATTTCTGTAATTTTGGAGAAAGA 840
DB 541 TGGGATTGACACGATAAATCTCAATGAAATCTATAAAGAGATTTCTGTAATTTTGGAGAAAGA 600
QY 841 GAATATGCTGATCACTGTCGAATATGTAATCGGGGATTAATAAATTTACCGAAATCT 900
DB 601 GAATATGCTGATCACTGTCGAATATGTAATCGGGGATTAATAAATTTACCGAAATCT 660
QY 901 ACATATCAAGATTGGATTAACATTAATCGATTACGGAGAGACTTAAACATTTGACTGATTATTA 960
DB 661 ACATATCAAGATTGGATTAACATTAATCGATTACGGAGAGACTTAAACATTTGACTGATTATTA 720
QY 961 GATATCGCGCTTTCTTCCAACTATGCAATAGGAGATATCCAAATTCAGCAGTTGGT 1020
DB 721 GATATCGCGCTTTCTTCCAACTATGCAATAGGAGATATCCAAATTCAGCAGTTGGT 780
QY 1021 CAATTAACAAAGGAAGTTTATACGACCCATTAATTAATTTTAAATCCACAGTTACAGTCT 1080
DB 781 CAATTAACAAAGGAAGTTTATACGACCCATTAATTAATTTTAAATCCACAGTTACAGTCT 840
QY 1081 GTAGCTCAATTAACCTTACTTTTAAAGTTATGAGAGAGAGCCCAATTAAGAAATCTCTATTA 1140
DB 841 GTAGCTCAATTAACCTTACTTTTAAAGTTATGAGAGAGAGCCCAATTAAGAAATCTCTATTA 900
QY 1141 TTTGATATATGCAATTAATCTTACAATCTTTACGATTTGGTTAGTGTGGAGCGCATTTT 1200
DB 901 TTTGATATATGCAATTAATCTTACAATCTTTACGATTTGGTTAGTGTGGAGCGCATTTT 960
QY 1201 TATTGGGAGGACATCGAGTAATATCTAGCTTATAGGAGTGTGTAACATAACATCTCTCT 1260
DB 961 TATTGGGAGGACATCGAGTAATATCTAGCTTATAGGAGTGTGTAACATAACATCTCTCT 1020
QY 1261 ATATATGAGAGAGAGCGCAACAGGAGCTTCCAGATCTTTTACTTTTAAATGGACGGTA 1320
DB 1021 ATATATGAGAGAGAGCGCAACAGGAGCTTCCAGATCTTTTACTTTTAAATGGACGGTA 1080
QY 1321 TTTAGGACTTTTATCAATCTCTTACGATTTATACGATTTATACGACCACTTCCAGCGCACCA 1380
DB 1081 TTTAGGACTTTTATCAATCTCTTACGATTTATACGATTTATACGACCACTTCCAGCGCACCA 1140
QY 1381 TTTTAAATTTAGTGTGGTGAAGGATAGAAATTTTCTACACCTACAAATAGCTTTACGTAT 1440
DB 1141 TTTTAAATTTAGTGTGGTGAAGGATAGAAATTTTCTACACCTACAAATAGCTTTACGTAT 1200
QY 1441 GCAGAGAGGTAACGTTGATTTTAACTGAATTAACGCTGAGGATTAATAGTGTGCA 1500
DB 1201 GCAGAGAGGTAACGTTGATTTTAACTGAATTAACGCTGAGGATTAATAGTGTGCA 1260
QY 1501 CTTCCGAGGATATAGTCACTGTTTATGTCGAATCTTGTTCGAAATCTGGAACA 1560
DB 1261 CTTCCGAGGATATAGTCACTGTTTATGTCGAATCTTGTTCGAAATCTGGAACA 1320
QY 1561 CTTTAAATTAACCTGTTAGTATTTTCTGGAAGATCTGAGTGAATCTTACAAAT 1620
DB 1321 CTTTAAATTAACCTGTTAGTATTTTCTGGAAGATCTGAGTGAATCTTACAAAT 1380
QY 1621 ACAATTTGATCCAGAGAAATTAATCAATATCTTTTAAAGATTTAGAGTTGGGG 1680
DB 1381 ACAATTTGATCCAGAGAAATTAATCAATATCTTTTAAAGATTTAGAGTTGGGG 1440
QY 1681 GGCACCTCTGTCTATTACAGGACAGGATTTACAGGAGGGGATATCTTTCGAGAGAAATCC 1740

Db 1441 GGCACCTCTGTCATTACAGGACCGGATTTTACAGGAGGGGATATCTTTCGAGAAATACC 1500
QY 1741 TTTGGTGATTTTGTATCTCTCAAGTCAATATTAATTCACCAATTAACCCAAAGATACCGT 1800
Db 1501 TTTGGTGATTTTGTATCTCTCAAGTCAATATTAATTCACCAATTAACCCAAAGATACCGT 1560
QY 1801 TTAAGATTTCGTTACGCTTCAGTAGGATGCGAGTATATAGTATTAACAGAGCGGCA 1860
Db 1561 TTAAGATTTCGTTACGCTTCAGTAGGATGCGAGTATATAGTATTAACAGAGCGGCA 1620
QY 1861 TCCACAGGAGTGGAGGCCCAAGTTAGTGTAGATATGCTCTTCAGAAAATCTATGGAATA 1920
Db 1621 TCCACAGGAGTGGAGGCCCAAGTTAGTGTAGATATGCTCTTCAGAAAATCTATGGAATA 1680
QY 1921 GGGGAGAACTTAACTATAGAACTTTAGATATACCGATTTTATAGTATCTCTTTTCATTT 1980
Db 1681 GGGGAGAACTTAACTATAGAACTTTAGATATACCGATTTTATAGTATCTCTTTTCATTT 1740
QY 1981 AGAGCTAATCCAGATATATTTGGGATAAGTGAACAACCTCTATTTGGTGAGGTTCTATT 2040
Db 1741 AGAGCTAATCCAGATATATTTGGGATAAGTGAACAACCTCTATTTGGTGAGGTTCTATT 1800
QY 2041 AGTAGCGTTGAACTTTATATAGATAAAATTTGAAATTTATCTAGCAGATGCAACATTTGAA 2100
Db 1801 AGTAGCGTTGAACTTTATATAGATAAAATTTGAAATTTATCTAGCAGATGCAACATTTGAA 1860
QY 2101 GCAGAACTCTGATTTAGAAAGAGACAAAAGCGGTGAATGCCCTGTTTACTTCTTCCAAAT 2160
Db 1861 GCAGAACTCTGATTTAGAAAGAGACAAAAGCGGTGAATGCCCTGTTTACTTCTTCCAAAT 1920
QY 2161 CAAATCGGTTAAACCGATGAGCGGATATCATATTTGATCAAGATGTCCTTCCATTTAGTG 2220
Db 1921 CAAATCGGTTAAACCGATGAGCGGATATCATATTTGATCAAGATGTCCTTCCATTTAGTG 1980
QY 2221 GATTGTTATCATGATGATTTCTGCTGGATGAAAGCGGAGATTTGTCGAGAAAGTCAAA 2280
Db 1981 GATTGTTATCATGATGATTTCTGCTGGATGAAAGCGGAGATTTGTCGAGAAAGTCAAA 2040
QY 2281 CATGCGAAGCGACTCAGTGATGAGCGGATTTACTTCAAGATCCAACTTCAGAGGGATC 2340
Db 2041 CATGCGAAGCGACTCAGTGATGAGCGGATTTACTTCAAGATCCAACTTCAGAGGGATC 2100
QY 2341 AATAGCAACCGACCGTGGCTGGAGGAGATGACAGATATTTACCATCCAAAGGAGAT 2400
Db 2101 AATAGCAACCGACCGTGGCTGGAGGAGATGACAGATATTTACCATCCAAAGGAGAT 2160
QY 2401 GACGTATTCAGAGAAATACGTCACACTACCGGTACCGTTGATGAGTCTATCCAAAG 2460
Db 2161 GACGTATTCAGAGAAATACGTCACACTACCGGTACCGTTGATGAGTCTATCCAAAG 2220
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Db 2221 TATTTATATCAGAAAATAGATGATGCGAAATTTAAAGCTTTATACCGGTTATGAATTAAGA 2280
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Db 2341 GAAATAGTAAATGTCGACGCGGCTCTTATGCGCGCTTCAGCCCAAGTCCAATC 2400
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QY 2701 TGTTCTCGAG 2711
Db 2461 TGTTCTCGAG 2471

; Sequence 1, Application US/08757536
; Patent No. 5942664
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Gilmer, Amy Jelen
; APPLICANT: Mettus, Anne-Marie Light
; TITLE OF INVENTION: Bacillus thuringiensis CryIC
; TITLE OF INVENTION: Compositions Toxic to Lepidopteran Insects and Methods for
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White and Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,536
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MOBT:023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3567 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3567
; US-08-757-536-1

Query Match 89.6%; Score 2429.4; DB 2; Length 3567;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 241 ATGGAGGAAAATAATCAAAATCAATGCATACCTTCAATTTGTTTAAAGTAATCCTGAAGAA 300
Db 1 ATGGAGGAAAATAATCAAAATCAATGCATACCTTCAATTTGTTTAAAGTAATCCTGAAGAA 60
QY 301 GTACTTTTGGATGGAGAACGGATATCAACTGTAATTAATCAATGATATTTCTCTGTCA 360
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Db 301 GGATTTAGGAAACAATTTTCAATATATATCTGGAAGCATTTTAAAGATGGGAAGATCCT 360
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2341 GAATAGTAAATGTCGAGGACCGGTTCTTATGCGGCTTTCAGCCCAAGTCCAATC 2400
2641 GGAAGTGTGAGAAACCGATCGATCGCCACACCTTGAATGAATCTCTGATCTAGAT 2700
2401 GGAAGTGTGAGAAACCGATCGATCGCCACACCTTGAATGAATCTCTGATCTAGAT 2460
2701 TGTCTCTGAG 2711
2461 TGTCTCTGAG 2471

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;; Sequence 11, Application US/08757536
;; Patent No. 5942664
;; GENERAL INFORMATION:
;; APPLICANT: Baum, James A.
;; APPLICANT: Gilmer, Amy Jelen
;; APPLICANT: Mettus, Anne-Marie Light
;; TITLE OF INVENTION: Bacillus thuringiensis CryIC
;; TITLE OF INVENTION: Compositions Toxic to Lepidopteran Insects and Methods for
;; TITLE OF INVENTION: Making CryIC Mutants
;; NUMBER OF SEQUENCES: 57
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White and Durkee
;; STREET: P.O. Box 4433
;; CITY: Houston
;; STATE: TX
;; COUNTRY: USA
;; ZIP: 77210-4433
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/757,536
;; FILING DATE: CONCURRENTLY HERewith
;; CLASSIFICATION: 800
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kitchell, Barbara
;; REGISTRATION NUMBER: 33,928
;; REFERENCE/DOCKET NUMBER: MOBT:023
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (512) 418-3000
;; TELEFAX: (512) 474-7577
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3567 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..3567
;; US-08-757-536-11

Query Match 89.6%; Score 2429.4; DB 2; Length 3567;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 241 ATGGAGGAAATAATCAAAATCAATGCATACCTTACAAATGTTTAAAGTAATCCTGAAGAA 300
DB 1 ATGGAGGAAATAATCAAAATCAATGCATACCTTACAAATGTTTAAAGTAATCCTGAAGAA 60

QY 301 GTACTTTTCGATCGGAGACCGATATCAACTGGTAATTAATCAATGATATTTCTCTGTCA 360
DB GTACTTTTCGATCGGAGACCGATATCAACTGGTAATTAATCAATGATATTTCTCTGTCA 120

QY 361 CTGTGTCAGTTCTGTTCTAACTTTGTACAGAGGGGAGGATTTTGTAGTGGATTAATA 420
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QY 421 GATTTTGTATGGGAATAGTGTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATGAA 480
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QY 481 CAATTAATTAAGAAAGATAGTGTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAAT 540
DB CAATTAATTAAGAAAGATAGTGTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAAT 300

QY 541 GGATAGGAAAACAATTTCAATATATATGTGGAAGCAATTTAAAGAAATGGAAGATCCT 600
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QY 601 AATAATCCAGCAACAGGACAGAGTAATTGATCGCTTCGTATATCTTGTGATGGGCTACTT 660
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DB 361 CATAATCCAGCAACAGGACAGAGTAATTGATCGCTTCGTATATCTTGTATGGGCTACTT 420
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DB 421 GAAAGGGACATTCCTTCGTTTCGAATTTCTGGAATTTGAAGTACCCCTTTTATCCGTTTAT 480
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DB 721 GATATCGCGCTTCTTTCGCAAACTATGACAAATAGAGATATCCAAATTCAGCCAGTTGT 780
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DB 781 CAACCTAACAGGGAAGTTTATACGCAACCAATTAATTTTAAATCCACAGTTACAGTCT 840
QY 1081 GTAGCTCAATTACCTACTTCTTAAACGTTATGAGAGACAGCGCAATTAGAAATCCTCATTTA 1140
DB 841 GTAGCTCAATTACCTACTTCTTAAACGTTATGAGAGACAGCGCAATTAGAAATCCTCATTTA 900
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DB 1741 GGCACTCTGTCTATTAAGGACAGGATTTTACAGGAGGATATCTTTCGAGAAATATACC 1740
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us-09-918-485-1.rni

Wed Oct 15 11:56:11 2003

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2101 AATAGACAAACAGACCGTGGCTGGAGAGGAAGTACAGATATTAATTCATCCAGAGGAGAT 2160
2401 GACGTATTTCAAGAGATTTACGTCACTACCGGTACCGTTGATGATGCTATCCAAG 2460
2161 GACGTATTTCAAGAGATTTACGTCACTACCGGTACCGTTGATGATGCTATCCAAG 2220
2461 TATTTATATCAGAAATAGATGAGTGCAGAAATTTAAAGCTTATACCGGTTATGAATTAAGA 2520
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2701 TGTTCCTGCAG 2711
2461 TGTTCCTGCAG 2471

Query Match      89.6%; Score 2429.4; DB 3; Length 3567;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 241 ATGAGGAAATTAATCAAAATCAATGATCACTTCAATCTGATTAATCAATCTGATTAATCTCTGCA 360
DB 1 ATGAGGAAATTAATCAAAATCAATGATCACTTCAATCTGATTAATCAATCTGATTAATCTCTGCA 60
QY 301 GTACTTTTGGATGAGAGGAGATCACTGATTAATCAATCTGATTAATCAATCTGATTAATCTCTGCA 360
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DB 301 GGATTTAGGAAACAAATTTCAATATATATGATGAAGATAGTGAATTTGATTAATGAAGATAGTGA 360

Sequence 1, Application US/09314093
Patent No. 6033874
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Gilmer, Amy Jelen
APPLICANT: Mettus, Anne-Marie Light
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
TITLE OF INVENTION: LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: /09/314,093
APPLICATION NUMBER: US/09/314,093
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/980,071
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURES:
NAME/KEY: CDS
LOCATION: 1..3567
US-09-314-093-1
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RESULT 13
US-09-314-093-1

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QY 1381 TTATTTTACGTTGGTGAAGAGTAAATTTTCTACACCTTACAAATAGCTTTAGGTAT 1440
DB 1141 TTATTTTACGTTGGTGAAGAGTAAATTTTCTACACCTTACAAATAGCTTTAGGTAT 1200
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DB 1261 CCTCGGAAAGGATATAGTTCATCGTTTATGTCATGCAACTTTTGTTCAAAGATCTGGAAACA 1320
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DB 1381 ACAAATGATCCAGAGAGATTAATCAATACCTTTTGTGAAAGGATTTAGGTTTGGGG 1440

QY 1681 GGCACCTCTGTCAATTAAGAGACCAAGATTTACAGGAGGGATATCTTCCAGAAATATACC 1740
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QY 1801 TTAAGATTTTCGTTTACGCTTCCAGTAGGAGTGCAGCAGTTATAGTATTTAACAGGAGCGGA 1860
DB 1561 TTAAGATTTTCGTTTACGCTTCCAGTAGGAGTGCAGCAGTTATAGTATTTAACAGGAGCGGA 1620
QY 1861 TCCACAGGAGTGGGAGCCAAAGTTAGTGTAGATATATCCCTCTTTCAGAAAACTATGGAATA 1920
DB 1621 TCCACAGGAGTGGGAGCCAAAGTTAGTGTAGATATATCCCTCTTTCAGAAAACTATGGAATA 1680
QY 1921 GGGGAGAACTTAACTATAGAACATTTAGATATACCGATTTTAGTAATCCTTTTTCATTT 1980
DB 1681 GGGGAGAACTTAACTATAGAACATTTAGATATACCGATTTTAGTAATCCTTTTTCATTT 1740
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QY 2101 GCAGAACTCTGATTTTGAAGAGACCAAAAGGGGGTGAATGCCCTGTTTACTTCTTCCAAAT 2160
DB 1861 GCAGAACTCTGATTTTGAAGAGACCAAAAGGGGGTGAATGCCCTGTTTACTTCTTCCAAAT 1920
QY 2161 CAAATCGGGTTAAAAACCGATGTGACGATATCATATTTGATCAAGTATCCAAATTTAGTG 2220
DB 1921 CAAATCGGGTTAAAAACCGATGTGACGATATCATATTTGATCAAGTATCCAAATTTAGTG 1980
QY 2221 GATTTGTTATCAGATGAAATTTTGTCTGGATGAAAGCGAGAAATTTGTCGAGAAAGTCAAA 2280
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DB 2041 CATGCGAAGCGACTCAGTGATGAGCGGAAATTTACTTCAAGATCCAAACTTTCAGAGGGATC 2100
QY 2341 AATAGACAACAGACCGCTGGCTGGAGAGAGTACAGATATTTACCATCCAAAGAGGAGAT 2400
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QY 2401 GACGTATTTCAAAGAGAAATTAAGTCACTACCGGGTACCGTTGATGAGTGTCTATCCAAAG 2460
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DB 2461 TGTTCCTGCAG 2471


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RESULT 14
US-09-314-093-11
; Sequence 11: Application US/09314093
; Patent No. 603874
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Gilmet, Amy Jelen
; APPLICANT: Mettus, Anne-Marie Light
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
; TITLE OF INVENTION: LEPIOPTERAN-ACTIVE-DELTA-ENDOTOXINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/314,093
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/980,071
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MECO:206
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3567 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3567
US-09-314-093-11

Query Match 89.6%; Score 2429.4; DB 3; Length 3567;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Qy 1981 AGAGCTAATCCAGATATAATTTGGATAAGTGAACACCTCTATTTGTCGAGGTTCTATT 2040

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Db 1981 GATTTGTTATCAGATGAATTTTGTCTGAGTGAAGGAGAAATTTGTCGAGAAAGTCAAA 2040

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Db 2041 CATGCAAGGACTCAGTATGAGCGGAATTTACTTCAAGATCCAACTTCAGAGGATC 2100

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Db 2101 AATAGACAACCGACCGTGGAGGAGGATGACAGATATTTACCATCCAGGAGAT 2160

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Qy 2701 TGTCTCTGCAG 2711

Db 2461 TGTCTCTGCAG 2471

RESULT 15

US-08-933-891-5

; Sequence 5, Application US/08933891

; Patent No. 6096708

; GENERAL INFORMATION:

; APPLICANT: Payne, Jewel M.

; APPLICANT: Sick, August J.

; TITLE OF INVENTION: No. 6096708el Bacillus thuringiensis Isolate

; TITLE OF INVENTION: Active Against Lepidopteran Peats, and Genes Encoding

; TITLE OF INVENTION: No. 6096708el Lepidopteran-Active Toxins

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Saliwanchik & Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: FL

; COUNTRY: US

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/933,891

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/356,034

; FILING DATE:

; APPLICATION NUMBER: US/08/210,110

; FILING DATE:

; APPLICATION NUMBER: 07/865,168

; FILING DATE: 09-APR-92

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/451,261

; FILING DATE: 14-DEC-89

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/371,955

; FILING DATE: 27-JUN-89

; ATTORNEY/AGENT INFORMATION:

; NAME: Saliwanchik, Roman

; REGISTRATION NUMBER: 21,023

; REFERENCE/DOCKET NUMBER: MA43.C1.D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (904)375-8100

; TELEFAX: (904)372-5800

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3567 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: BACILLUS THURINGIENSIS

; STRAIN: AIZAWAI

; INDIVIDUAL ISOLATE: PS811

; IMMEDIATE SOURCE:

; LIBRARY: LAMBDA GEM (TM) - 11 LIBRARY OF AUGUST SICK

; CLONE: 811B2

US-08-933-891-5

Query Match 89.6%; Score 2429.4; DB 3; Length 3567;

Best Local Similarity 98.9%; Pred. No. 0;

Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Qy 781 TTGGGATTCAGAACGATTAATCTCAATGAAGAACTATTAATAGACTCTGTAATTTAGGCAATTCAT 840
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Qy 2461 TGTTCCTGCAG 2471
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Job time : 242 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2003, 22:40:15 ; Search time 855 Seconds
(without alignments)
8559.271 Million cell updates/sec

Title: US-09-918-485-1

Perfect score: 2711

Sequence: 1 AAGCTTCAATAGAACTCAA.....GATCTAGATTGTCCTGCAG 2711

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_19Jun03.*

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20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2695	99.4	2711	9 AAN81949	Encodes delta endo
2	2688.2	99.2	2711	9 AAN81242	Sequence of a 3kb
3	2664	99.3	3223	12 AAQ10229	Sequence encoding
4	2432.6	89.7	3567	12 AAQ10181	Lepidopteran-activ
5	2431	89.7	3567	16 AAQ80646	CryIC gene. Bacil
6	2429.4	89.6	3567	14 AAQ47294	Delta endotoxin ge
7	2429.4	89.6	3567	19 AAV27848	DNA encoding a mut
8	2429.4	89.6	3567	19 AAV27843	DNA encoding a mut

9	2429.4	89.6	3567	20 AAX80039	B. thuringiensis c
10	2429.4	89.6	3567	20 AAX80019	B. thuringiensis c
11	2429.4	89.6	3567	21 AAA08144	Bacillus thuringie
12	2429.4	89.6	3567	21 AAA08149	Bacillus thuringie
13	2429.4	89.6	3567	24 AAD44210	Bacillus thuringie
14	2429.4	89.6	3567	24 AAD44215	Bacillus thuringie
15	2429.4	89.6	3567	24 ABS70781	B. thuringiensis D
16	2429.4	89.6	3567	24 ABS70786	B. thuringiensis D
17	2427.8	89.6	3567	19 AAV27845	DNA encoding a mut
18	2427.8	89.6	3567	19 AAV27847	DNA encoding a mut
19	2427.8	89.6	3567	19 AAV27844	DNA encoding a mut
20	2427.8	89.6	3567	20 AAX80036	B. thuringiensis c
21	2427.8	89.6	3567	20 AAX80038	B. thuringiensis c
22	2427.8	89.6	3567	20 AAX80020	B. thuringiensis c
23	2427.8	89.6	3567	21 AAA08145	Bacillus thuringie
24	2427.8	89.6	3567	21 AAA08146	Bacillus thuringie
25	2427.8	89.6	3567	21 AAA08148	Bacillus thuringie
26	2427.8	89.6	3567	24 AAD44211	Bacillus thuringie
27	2427.8	89.6	3567	24 AAD44212	Bacillus thuringie
28	2427.8	89.6	3567	24 AAD44214	Bacillus thuringie
29	2427.8	89.6	3567	24 ABS70782	B. thuringiensis D
30	2427.8	89.6	3567	24 ABS70783	B. thuringiensis D
31	2427.8	89.6	3567	24 ABS70785	B. thuringiensis D
32	2426.2	89.5	3567	19 AAV27846	DNA encoding a mut
33	2426.2	89.5	3567	20 AAX80037	B. thuringiensis c
34	2426.2	89.5	3567	21 AAA08147	Bacillus thuringie
35	2426.2	89.5	3567	24 AAD44213	Bacillus thuringie
36	2426.2	89.5	3567	24 ABS70784	B. thuringiensis D
37	2421.4	89.3	3567	22 AAS08951	Bacillus thuringie
38	2419.8	89.3	3567	19 AAV27863	DNA encoding a mut
39	2419.8	89.3	3567	20 AAX80004	EG12111 crystal pr
40	2419.8	89.3	3567	21 AAA08166	Bacillus thuringie
41	2419.8	89.3	3567	24 AAD44232	Bacillus thuringie
42	2419.8	89.3	3567	24 ABS70803	B. thuringiensis D
43	2418.2	89.2	3567	19 AAV27864	DNA encoding a mut
44	2418.2	89.2	3567	20 AAX80005	EG12121 crystal pr
45	2418.2	89.2	3567	21 AAA08167	Bacillus thuringie

ALIGNMENTS

RESULT 1	
AAN81949	
ID AAN81949 standard; cDNA; 2711 bp.	
XX	
AC AAN81949;	
XX	
DT 25-MAR-2003 (updated)	
DT 23-OCT-1990 (first entry)	
XX	
DE Encodes delta endotoxin active against Lepidoptera larvae.	
XX	
KW Lepidoptera larvae; insecticide; Bacillus thuringiensis;	
KW Spodoptera littoralis; ss.	
XX	
OS synthetic.	
XX	
FH Key	Location/Qualifiers
FT CDS	241..2711
FT	/*tag= a
FT	/product=insecticidal polypeptide
XX	
PN WO8809812-A.	
XX	
PD 15-DEC-1988.	
XX	
PF 09-JUN-1988; 88WO-FR00292.	
XX	
PR 10-JUN-1987; 87FR-0008090.	
PR 06-MAY-1988; 88EP-0401121.	
XX	
PA (INSP) INST PASTEUR.	

(INRG) INST NAT RECH AGRONOMIQ.
 Sanchis V, Lereclus D, Menou G;
 WPI: 1988-368627/51.
 P-PSDB; AAP81502.
 XX New nucleotide sequences encoding new polypeptide -
 PT with selective action against lepidopteran larvae esp Spodoptera
 PT littoralis
 XX
 PS Claim 9, Page 47; 65pp; French.
 XX
 CC The sequence is derived from a 3kb HindIII-PstI fragment of
 CC Bacillus thuringiensis. Recombinant sequences can also be
 CC constructed from 2 diff strains of B. thuringiensis. The sequence
 CC between bases 50 to 95 is claimed separately as this encodes at
 CC least a part of the N-terminal region of an insecticidal
 CC polypeptide. There is a variable nucleotide at posn 611 which is C
 CC in the sequence given here but which is A in the shorter sequence.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct DR field.)
 CC
 XX SQ Sequence 2711 BP; 877 A; 442 C; 560 G; 832 T; 0 other;
 Query Match 99.4%; Score 2695; DB 9; Length 2711;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 2701; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 1 AAGCTTCAATAGATCTCAATCTCGATGACTCTGTTAGTCTTTTATATCTGCTACTTG 60
 1 AAGCTTCAATAGATCTCAATCTCGATGACTCTGTTAGTCTTTTATATCTGCTACTTG 60
 61 ACAGGGGTAGGAACATAATCGGTCAATTTAATATGAGGCAATATGATTTATAA 120
 61 ACAGGGGTAGGAACATAATCGGTCAATTTAATATGAGGCAATATGATTTATAA 120
 121 AATTTGTTACGTTTGTATTTTTCATAGATGTTGTCATATGATTTAATCGTGTAA 180
 121 AATTTGTTACGTTTGTATTTTTCATAGATGTTGTCATATGATTTAATCGTGTAA 180
 181 TGAAGAACAGTATCAAACTATCAGAACTTTGTTAGTTTAAATAAAAAACGAGGATTTT 240
 181 TGAAGAACAGTATCAAACTATCAGAACTTTGTTAGTTTAAATAAAAAACGAGGATTTT 240
 241 ATGAGGAAATATCAAAATCAATGATACCTTACAAATTTTAAAGTAAATCTGTAAGAA 300
 241 ATGAGGAAATATCAAAATCAATGATACCTTACAAATTTTAAAGTAAATCTGTAAGAA 300
 301 GTACTTTTGGATGGAGAACGATATCACTGTTAATCTCAATGATATTTCTCTGTCA 360
 301 GTACTTTTGGATGGAGAACGATATCACTGTTAATCTCAATGATATTTCTCTGTCA 360
 361 CTGTTTCACTTTCTGTTATCTTAATTTGTACCGGGGAGGATTTTAAAGTTGAATTAATA 420
 361 CTGTTTCACTTTCTGTTATCTTAATTTGTACCGGGGAGGATTTTAAAGTTGAATTAATA 420
 421 GATTTTGTATGGGAATAGTGGCCCTCTCAATGGGATGATTTCTAGTACAAATGAA 480
 421 GATTTTGTATGGGAATAGTGGCCCTCTCAATGGGATGATTTCTAGTACAAATGAA 480
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 1321 TTTAGGACTTTATCAATTTCTTCTTTACGATTTATACAGCAACTTTGCGAGCGCCAT 1380
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Db	1741	TTTTGGTGATTTTGTATCTCTACAGTCAATATTAATTCACAAATTACCCAAAGATACCGT	1800
Qy	1801	TTAAGATTTTCGTTACGCTCCAGGTAGGATGCGACAGTTATAGTATTAAACAGAGCGGCA	1860
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Qy	1861	TCCA CAGAGTGGGAGGCCAAAGTTAGTGTAGATATGCCTCTTCAGAAAACTATGGAATA	1920
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Qy	1921	GGGGAGAACCTTACATCTAGAACATTTAGATATACCGATTTTATGTAATCTCTTTTCA	1980
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Qy	1981	AGAGCTTAATCCAGATATAAATGGGATAAGTGAAACAACCTCTATTGGTGACAGTCTTAT	2040
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Qy	2041	AGTAGCGTTGAACTTTATATAGATAAAATTTGAAATTAATTTACAGATGCAACAATTTGAA	2100
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Db	2161	CAAAATCGGGTTAAAAACCGATGTGACGGATTAATCATATTGATCAAGTATCCAAATTTAG	2220
Qy	2221	GATTGTTTATCAGATGAATTTTGTCTGGATGAAAAAGCGAGAAATGTCCGAGAAAGTCAA	2280
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Qy	2281	CATTGCGAAGCGACTCAGTGATGACGGAATTTACTTTCMAAGATCCAAACTTCAGAGGATC	2340
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Db	2341	AATAGACAACCCAGACCGTGGCTGGAGAGGAAGTACAGATATTACCATCCAAGAGGAGAT	2400
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Db	2401	GACGTATTCAAAGAGAAATTACGTCACTACCGGGTACCGTTGATGAGTGCTATCCAAG	2460
Qy	2461	TATTTATATCAGAAAAATAGATGAGTCGAAATTAAGAGCTTATACCCGTTATGAATTAAG	2520
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Qy	2521	GGGTATATCGAAGATAGTCAAGACTTAGAAAACTATTTGATCGCGTACAAATCGAAACAC	2580
Db	2521	GGGTATATCGAAGATAGTCAAGACTTAGAAAACTATTTGATCGCGTACAAATCGAAACAC	2580
Qy	2581	GAAATAGTAATCTGCCAGGCA CGGGTTCTTATGGCGCTTTCAGGCCCAAGTCCAATC	2640
Db	2581	GAAATAGTAATCTGCCAGGCA CGGGTTCTTATGGCGCTTTCAGGCCCAAGTCCAATC	2640
Qy	2641	GGAAAGTGTGGAAACCGAATCGATCGCGCCACACTTTGAATGGHAATCTGATCTAGAT	2700
Db	2641	GGAAAGTGTGGAAACCGAATCGATCGCGCCACACTTTGAATGGHAATCTGATCTAGAT	2700
Qy	2701	TGTTCTCTGCAG 2711	
Db	2701	TGTTCTCTGCAG 2711	

RESIST 2

RESULT 2
AAN81242

AA81242
ID AAN81242 standard; DNA; 2711 BP.

XX

AAN81242:

	25-MAR-2003	(updated)
	30-OCT-1990	(first entry)
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100	100	100

Sequence of a 3kb Hind III-Pst I fragment of *Bacillus thuringiensis* (BT) strain aizawai 7-29 and entomocidus 6-01.

Microbial insecticide; pesticide; bacterium; Noctuellae;
Spodoptera littoralis; Mamestra brassicae; ss.

Bacillus thuringiensis.

EP295156-A.

14-DEC-1988.

06-MAY-1988: 88EP-0401121.

10--JUN-1987: 87ER-0008090-

(INSP) INST PASTEUR.

(CNRS) CENT NAT RECH SCI.

(INRG) INRA INST NAT RECH AGRONOMIQUE.

Sanchis V, Lereclus D, Menou G, Lecadet MM, Martouret D, Dedonder R;
WPI; 1988-355565/50.

New DNA sequences encoding insecticidal polypeptide -
with specific activity against lepidoptera larvae esp.
Spodoptera littoralis

Claim 9; Pages 23-25; 37pp; French.

It can hybridise with 3 specified probes from the gene of BT crystal protein. It is particularly derived from the BT, or by *in vitro* genetic recombination of DNA fragments from 2 different BT strains, esp. aizawai 7-29 deposited as CNCM I-561 or I-660, resp. It encodes at least part of the N-terminal region of a polypeptide which is specifically toxic for lepidopteran larvae of family Noctuellae (esp. *Spodoptera littoralis*). It can be used to express polypeptides which are used as insecticides (against *S. littoralis* or *Manesstra brassicae*). may also be incorporated directly in plants or micro-organisms, pref. *Pseudomonas*, *Azospirillum* or *Rhizobium*, which live in the plant environment.
(Updated on 25-MAR-2003 to correct PA field.)

Sequence 2711 BP; 873 A; 443 C; 563 G; 831 T; 1 other;

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Query Match          99.2%; Score 2688.2; DB 9; Length 2711;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2696; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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Db 2 AGCTTCAATAGAAATCTCAAAATCTCGATGACTGCTTAGTCTTTTAAATACTGTCTACCTGA 61

QY 62 CAGGGGTAGGAACATAATCGGTCAATTTTAAATATGGGGCATATATTGATATTTTATAAA 121

Db 62 CAGGGGTAGGAACATAATCGGTCAATTTTAGGTATGGGGCGGTATA TTGATATTTTATAAA 121

OV 122 ATTGTGTTACGTTTUTGTATTUTTTTCATAAGATGTGTCTATATGTATTAAATCGTGCGTAAT 181

Db 122 ATTGTGTTACGTTTTTGTATTTTTCATAAGATGTGTCTATGTATTAAATCGTGGAAT 181

182 GAAAAACAGTATCAAACTATCAGAACTTTGGTAGTTTAAATAAAAAACGACGCTATTTTAA 241

183 182 181 180 179 178 177 176 175 174 173 172 171 170 169 168 167 166 165 164 163 162 161 160 159 158 157 156 155 154 153 152 151 150 149 148 147 146 145 144 143 142 141 140 139 138 137 136 135 134 133 132 131 130 129 128 127 126 125 124 123 122 121 120 119 118 117 116 115 114 113 112 111 110 109 108 107 106 105 104 103 102 101 100 99 98 97 96 95 94 93 92 91 90 89 88 87 86 85 84 83 82 81 80 79 78 77 76 75 74 73 72 71 70 69 68 67 66 65 64 63 62 61 60 59 58 57 56 55 54 53 52 51 50 49 48 47 46 45 44 43 42 41 40 39 38 37 36 35 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

[illegible]

243

302	QY	TAC	TTTTGGATGGAGAACGGATATCAACTGGTAAATTA	CTCAAA	TGATATATTTCTCTGTCCAC	361
302	DB	TAC	TTTTGGATGGAGAACGGATATCAACTGGTAAATTA	CTCAAA	TGATATATTTCTCTGTCCAC	361
362	QY	TGT	TTTCAGTTCTCTGATATCTA	CTAACTTTGT	PACACGGGGAGGATTTTTAGTTGGATTAATAG	421
362	DB	TGT	TTTCAGTTCTCTGATATCTA	CTAACTTTGT	PACACGGGGAGGATTTTTAGTTGGATTAATAG	421
422	QY	ATT	TTGTATGGGNA	TAGTTGGCCCTTCTCAATGGGATGCATTTCTAGTACAAATTTGAAC	481	
422	DB	ATT	TTGTATGGGNA	TAGTTGGCCCTTCTCAATGGGATGCATTTCTAGTACAAATTTGAAC	481	
482	QY	AAT	TAATTAATGAAGAA	TAGCTGAAATTTCTGTAGNAAGCTGCTATTGCTTAATTTAGAG	541	
482	DB	AAT	TAATTAATGAAGAA	TAGCTGAAATTTCTGTAGNAAGCTGCTATTGCTTAATTTAGAG	541	
542	QY	GAT	TAGGAAACAA	TTTCAATATATATGTGTGAACCATTTAAGAA	TGGGAGAGATCTTA	601
542	DB	GAT	TAGGAAACAA	TTTCAATATATATGTGTGAACCATTTAAGAA	TGGGAGAGATCTTA	601
602	QY	ATA	ATCCAGCAACACAGACACAGATTAAT	TGATGCTTTCGTATAC	TTTGATGGGCTACTTG	661
602	DB	ATA	ATCCAGCAACACAGACACAGATTAAT	TGATGCTTTCGTATAC	TTTGATGGGCTACTTG	661
662	QY	AA	GAGGACATTCCTTCGTTTCGAAATTTCTGGAATTTCAAGTACCCCTTTTATCCGTTTATG			721
662	DB	AA	GAGGACATTCCTTCGTTTCGAAATTTCTGGAATTTCAAGTACCCCTTTTATCCGTTTATG			721
722	QY	CT	CAAGCGCCCAATCTGCATCTAGCTATATTAATGAAGATTTCTGTAATTTTGGAGAAAGAT			781
722	DB	CT	CAAGCGCCCAATCTGCATCTAGCTATATTAATGAAGATTTCTGTAATTTTGGAGAAAGAT			781
782	QY	TG	GGATTTGACCAACGATAAATGTCAATGAAACTATAATAGACTAATTAGGCAATTTGATG			841
782	DB	TG	GGGATTTGACAACGATAAATGTCAATGAAACTATAATAGACTAATTAGGCAATTTGATG			841
842	QY	AAT	TGCTGATCCTGTGCAAAATAGTATATATCGGGATTTAAATATTTACCGAAATCTA			901
842	DB	AAT	TGCTGATCCTGTGCAAAATAGTATATATCGGGATTTAAATATTTACCGAAATCTA			901
902	QY	CG	TATCMAGATTTGATTAACATATATCGAATACGAGAGACTTTACATTTGACTGTATTAG			961
902	DB	CG	TATCMAGATTTGATTAACATATATCGAATACGAGAGACTTTACATTTGACTGTATTAG			961
962	QY	AT	TGCGCGCTTTCTTTCCAACTATGACATAGAGATATCCAAATTCAGCAGTTGGTC			1021
962	DB	AT	TGCGCGCTTTCTTTCCAACTATGACATAGAGATATCCAAATTCAGCAGTTGGTC			1021
1022	QY	A	CTAACAGGAGATTTATACGGACCCATTAATTAATTTTAATCCACAGTTACAGTCG			1081
1022	DB	A	CTAACAGGAGATTTATACGGACCCATTAATTAATTTTAATCCACAGTTACAGTCG			1081
1082	QY	TAG	CTCAATTCCTATCTTTTAAAGTTATGAGAGAGCGCAATTAAGAAATCCTCATTTAT			1141
1082	DB	TAG	CTCAATTCCTATCTTTTAAAGTTATGAGAGAGCGCAATTAAGAAATCCTCATTTAT			1141
1142	QY	TT	GATATATGGAATATCTTCAATCTTTACGGATTCGTTTATGTTGTGGAGCAATTTTT			1201
1142	DB	TT	GATATATGGAATATCTTCAATCTTTACGGATTCGTTTATGTTGTGGAGCAATTTTT			1201
1202	QY	ATT	GGGAGGACATCGAGTAAATCTAGCCTTTATAGGAGTGGTAAACATAATCTCTTA			1261
1202	DB	ATT	GGGAGGACATCGAGTAAATCTAGCCTTTATAGGAGTGGTAAACATAATCTCTTA			1261
1262	QY	TAT	TGGAAGAGAGCGCAACACAGAGCCCTCCAAAGATCCTTTACTTTTAAATGGACCGGTAT			1321
1262	DB	TAT	TGGAAGAGAGCGCAACACAGAGCCCTCCAAAGATCCTTTACTTTTAAATGGACCGGTAT			1321
1322	QY	TT	AGACTTTATCAATTCCTTACTTTTACGATTAATACAGCAACCTTGCCAGGCGCCACCAT			1381
1322	DB	TT	AGACTTTTATCAATTCCTTACTTTTACGATTAATACAGCAACCTTGCCAGGCGCCACCAT			1381
1382	QY	TT	TAATTTTACCTGCTGGTGAAGAGTAAATTTTCTACACCTTA	CAAAATAGCTTTACGTATG		1441

Db 2462 ATTATATCAGAAATAGATAGTCGAAATTAAGCTTATACCCGTTATGAATTAAGAG 2521

QY 2522 GGTATATCGAAGATAGTCAAGACTTAGAAATCTATTGTATCGGTACAATGCAAAACACG 2581

Db 2522 GGTATATCGAAGATAGTCAAGACTTAGAAATCTATTGTATCGGTACAATGCAAAACACG 2581

QY 2582 AAATAGTAATGTGCGAGCAGCGGTTCTTATATGCGCGCTTTTCAGCCCAAGTCCAAATCG 2641

Db 2582 AAATAGTAATGTGCGAGCAGCGGTTCTTATATGCGCGCTTTTCAGCCCAAGTCCAAATCG 2641

QY 2642 GAAAGTGTGAGAACCGAATCGATGCGCGCACACCTTGAATGGAATCTGTATCTAGATT 2701

Db 2642 GAAAGTGTGAGAACCGAATCGATGCGCGCACACCTTGAATGGAATCTGTATCTAGATT 2701

QY 2702 GTTCTGCGAG 2711

Db 2702 GTTCTGCGAG 2711

RESULT 3

AAQ10229

ID AAQ10229 standard; DNA; 3923 BP.

XX AAQ10229;

DT 25-MAR-2003 (updated)

DT 27-MAR-1991 (first entry)

XX

DE Sequence encoding insecticidal crystal protein (ICP) entomocidus

DE HD-110 of gene bt15.

XX

KW Insecticide; Lepidoptera; Coleoptera; ds.

XX

OS Bacillus thuringiensis.

XX

FH Key Location/Qualifiers

FT CDS 264..3761

FT /*tag= a

XX

PN EP408403-A.

XX

PD 16-JAN-1991.

XX

PF 29-MAY-1990; 90EP-0401427.

XX

PR 29-MAY-1990; 90EP-0401427.

XX

PR 31-MAY-1989; 89EP-0401499.

XX

PA (PLBZ) PLANT GENETICS SYSTEMS NV.

XX

PI Vannellaer H, Botterman J, Vanrie J, Joos H;

XX

DR WPI: 1991-016587/03.

DR P-PSDB; AAR10193.

XX

PT Insect-resistant transgenic plant cells - transformed with genes

PT encoding different non-competitively binding Bacillus

PT thuringiensis insecticidal proteins

XX

PS Disclosure; Fig 14; 82pp; English.

XX

CC Sequence may be used in transformation of crop plants, providing

CC resistance to insect (esp. lepidoptera and Coleoptera) attack,

CC without resort to insecticides which incur problems with development

CC of insect resistance

CC (Updated on 25-MAR-2003 to correct PA field.)

CC (Updated on 25-MAR-2003 to correct PI field.)

XX

SQ Sequence 3923 BP; 1304 A; 636 C; 849 G; 1134 T; 0 other;

Query Match 98.3%; Score 2664; DB 12; Length 3923;

Best Local Similarity 99.1%; Pred. No. 0;

Matches 2679; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 8 AATAGAACTCTCAAACTCTCGATGACCTCTTAGTCTTTTAAATCTGTCTACTTTGACAGGGG 67

Db 1 AATAGAACTCTCAAACTCTCGATGACCTCTTAGTCTTTTAAATCTGTCTACTTTGACAGGGG 60

QY 68 TAGGAACATAAATCGGTCAATTTTAAATATGGGGCATATATTGATATTTTATAAAATTTGT 127

Db 61 TAGGAACATAAATCGGTCAATTTTAAATATGGGGCATATATTGATATTTTATAAAATTTGT 120

QY 128 TACGTTTTTTTGTATTTTATCAAGATGTCTATGTATTAATCGTGTATGAAATAA 187

Db 121 TACGTTTTTTTGTATTTTATCAAGATGTCTATGTATTAATCGTGTATGAAATAA 180

QY 188 CAGTATCAAACTATCAGAACTTTTGTAGTTTAAATAAAAAACGGAGGTATTTTATCGAGG 247

Db 181 CAGTATCAAACTATCAGAACTTTTGTAGTTTAAATAAAAAACGGAGGTATTTTATCGAGG 240

QY 248 AAAATAATCAAAATCAATGCATACCTTACAAATGTTTAAAGTAATCTCTGAAGAAGTACTTT 307

Db 241 AAAATAATCAAAATCAATGCATACCTTACAAATGTTTAAAGTAATCTCTGAAGAAGTACTTT 300

QY 308 TGGATGGAGAACGATATCAACTGGTAAATTTACTCAATTCATATTTCTCTGTCTACCTGTTTC 367

Db 301 TGGATGGAGAACGATATCAACTGGTAAATTTCAATTCATATTTCTCTGTCTACCTGTTTC 360

QY 368 AGTTTTCTGTATCTAACTTTGTACCGGGGGAGGATTTTGTAGTTGGATTAATAGATTTTG 427

Db 361 AGTTTTCTGTATCTAACTTTGTACCGGGGGAGGATTTTGTAGTTGGATTAATAGATTTTG 420

QY 428 TATGGGAATAGTTGGCCCTCTCAATGGGATGCAATTTCTAGTACAAATGAACAATTA 487

Db 421 TATGGGAATAGTTGGCCCTCTCAATGGGATGCAATTTCTAGTACAAATGAACAATTA 480

QY 488 TTAATGAAGAAGTAGCTGAATTTGCTAGGAATGCTGCTATTCTCTAATTTAGAGGATTAG 547

Db 481 TTAATGAAGAAGTAGCTGAATTTGCTAGGAATGCTGCTATTCTAATTTAGAGGATTAG 540

QY 548 GAAACAATTTCAATATATATGTGGAAGCATTTTAAAGAATGGGAAGAAGATCCCTAATAATC 607

Db 541 GAAACAATTTCAATATATATGTGGAAGCATTTTAAAGAATGGGAAGAAGATCCCTAATAATC 600

QY 608 CAGCAACGAGACGAGATTAATGATCGCTTTTCGTATACCTGATGGGCTACTTGAAGGG 667

Db 601 CAGCAACGAGACGAGATTAATGATCGCTTTTCGTATACCTGATGGGCTACTTGAAGGG 660

QY 668 ACATTTCTTTCGTTTCGAAATTTCTGGAATTTGAAGTACCCCTTTTATCCGTTTATGCTCAAG 727

Db 661 ACATTTCTTTCGTTTCGAAATTTCTGGAATTTGAAGTACCCCTTTTATCCGTTTATGCTCAAG 720

QY 728 CGGCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTTCGAGAAAGATTTGGGAT 787

Db 721 CGGCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTTCGAGAAAGATTTGGGAT 780

QY 788 TGCAACGATAAATGTCATGAAATCTATAATAGACTAATTAAGGCATATTGATGAATATG 847

Db 781 TGCAACGATAAATGTCATGAAATCTATAATAGACTAATTAAGGCATATTGATGAATATG 840

QY 848 CTGATCACTGTGCAAAATACGTATATCGGGGATTAATAATTAATTCGGAATCTACGTATC 907

Db 841 CTGATCACTGTGCAAAATACGTATATCGGGGATTAATAATTAATTCGGAATCTACGTATC 900

QY 908 AAGATTGGATAACATATTAATCGATTACGAGAGACTTAACATTTGACTGTATTAGATATCG 967

Db 901 AAGATTGGATAACATATTAATCGATTACGAGAGACTTAACATTTGACTGTATTAGATATCG 960

QY 968 CGCTTTCTTTCCAAACTATGCAATAGAGATATCCAAATTCAGCCAGTTGGTCAACTAA 1027

Db 961 CGCTTTCTTTCCAAACTATGCAATAGAGATATCCAAATTCAGCCAGTTGGTCAACTAA 1020

QY 1028 CAAGGAAGTTTATACGGACCCCAATTAATTAATTTTAAATCCACAGTTACAGTCTGTAGCTC 1087

Db 1021 CAAGGAAGTTTATACGGACCCCAATTAATTAATTTTAAATCCACAGTTACAGTCTGTAGCTC 1080

QY	1088	AATTACCTA	1147	Db	2161	GGTTAAACCGAT	2220
Db	1089	AATTACCTA	1148	QY	2228	TATCAGATGA	2287
QY	1148	TATTGAATAT	1207	Db	2221	TATCAGATGA	2280
Db	1141	TATTGAATAT	1200	QY	2288	AGCGACTCAG	2347
QY	1208	GAGGACATC	1267	Db	2281	AGCGACTCAG	2340
Db	1201	GAGGACATC	1260	QY	2348	ACCAGAGCG	2407
QY	1268	GAAGAGGCG	1327	Db	2341	ACCAGAGCG	2400
Db	1261	GAAGAGGCG	1320	QY	2408	TCAGAGGAA	2467
QY	1328	CTTTATCAAT	1387	Db	2401	TCAGAGGAA	2460
Db	1321	CTTTATCAAT	1380	QY	2468	ATCAGAGAA	2527
QY	1388	TACGTGGTG	1447	Db	2461	ATCAGAGAA	2520
Db	1381	TACGTGGTG	1440	QY	2528	TCGAGATAG	2587
QY	1448	GAGGTAGCG	1507	Db	2521	TCGAGATAG	2580
Db	1441	GAGGTAGCG	1500	QY	2588	TAAATGTGC	2647
QY	1508	AAGGATATG	1567	Db	2581	TAAATGTGC	2640
Db	1501	AAGGATATG	1560	QY	2648	GTGGAGAAC	2707
QY	1568	TAAACACTG	1627	Db	2641	GTGGAGAAC	2700
Db	1561	TAAACACTG	1620	QY	2708	GCAG	2711
QY	1628	ATCCAGAGA	1687	Db	2701	GCAG	2704
Db	1621	ATCCAGAGA	1680	RESULT 4			
QY	1688	CTGTCAATC	1747	AAQ10181			
Db	1681	CTGTCAATC	1740	TD	AAQ10181	standard; DNA; 3567 BP.	
QY	1748	ATTTTGTAT	1807	XX	AAQ10181;		
Db	1741	ATTTTGTAT	1800	AC	25-MAR-2003	(updated)	
QY	1808	TTCGTTACG	1867	DT	20-MAR-1991	(first entry)	
Db	1801	TTCGTTACG	1860	XX	Lepidopteran-active toxin C gene (811B2).		
QY	1868	GAGTGGGCG	1927	DE	Lepidopteran-active toxin C; pest control; ss.		
Db	1861	GAGTGGGCG	1920	KW	Bacillus thuringiensis PS81L (NRRL B-18484).		
QY	1928	ACTTACATC	1987	OS	Bacillus thuringiensis PS81L (NRRL B-18484).		
Db	1921	ACTTACATC	1980	PN	EP405810-A.		
QY	1988	ATCCAGATAT	2047	PD	02-JAN-1991.		
Db	1981	ATCCAGATAT	2040	XX	18-JUN-1990; 90EP-0306594.		
QY	2048	TTGAACTTT	2107	XX	14-DEC-1989; 89US-0451261.		
Db	2041	TTGAACTTT	2100	PR	27-JUN-1989; 89US-0371955.		
QY	2108	CTGATTTAG	2167	XX	(MYCO) MYCOGEN CORP.		
Db	2101	CTGATTTAG	2160	PA	Payne J, Sick AJ;		
QY	2168	GGTTAAACCG	2227	PI	WPI; 1991-009132/02.		
				DR	P-PSDB; AAR10128.		
				XX	Bacillus thuringiensis contg. DNA encoding lepidopteran-active		
				PT	toxin - use of microorganisms transformed with the toxin gene		

PT in pest control
XX Claim 5; Page 19-23; 28pp; English.
XX Expression of the toxin gene by a host results, directly or
CC indirectly, in the intracellular prodn. and maintenance of the
CC pesticide.
CC See also AQ10179-82.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 3567 BP; 1168 A; 597 C; 791 G; 1011 T; 0 other;

Query Match 89.7%; Score 2432.6; DB 12; Length 3567;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2447; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 241 ATGGAGGAAATTAATCAAAATCAATGCATACCTTCAAAATGTTTAAAGTAATCTGAAGAA 300
DB 1 ATGGAGGAAATTAATCAAAATCAATGCATACCTTCAAAATGTTTAAAGTAATCTGAAGAA 60

QY 301 GTACTTTTGGATGGAGACGGATATCAACTGGTAAATTAATCAATGATATTTCTCTGTCA 360
DB 61 GTACTTTTGGATGGAGACGGATATCAACTGGTAAATTAATCAATGATATTTCTCTGTCA 120

QY 361 CTGTGTCAGTTTCTGTGATCTAATCTTTGTATCAAGGGGAGGATTTTGTGATTAATA 420
DB 121 CTGTGTCAGTTTCTGTGATCTAATCTTTGTATCAAGGGGAGGATTTTGTGATTAATA 180

QY 421 GATTTTGTATGGGATAGTTCGCCCTCTCAATGGGATGCAATTTCTAGTACAAATGAA 480
DB 181 GATTTTGTATGGGATAGTTCGCCCTCTCAATGGGATGCAATTTCTAGTACAAATGAA 240

QY 481 CAATTAATTAATGAAGAAATAGCTGAATTTGCTAGGAATGCTGCTAATTTAGAA 540
DB 241 CAATTAATTAATGAAGAAATAGCTGAATTTGCTAGGAATGCTGCTAATTTAGAA 300

QY 541 GGATAGGAAACAAATTTCAATATATATGTGGAAGCAATTAAGAAATGGGAAGATCCT 600
DB 301 GGATAGGAAACAAATTTCAATATATATGTGGAAGCAATTAAGAAATGGGAAGATCCT 360

QY 601 AATAATCCAGCAACAGGACAGAGTAATGTATCGCTTTTGTATCTTCAATCGGCTACTT 560
DB 361 AATAATCCAGCAACAGGACAGAGTAATGTATCGCTTTTGTATCTTCAATCGGCTACTT 420

QY 661 GAAAGGCAATTCCTTCGTTTCGAAATTTCTGGATTTGAAGTACCCCTTTTATCCGTTAT 720
DB 421 GAAAGGCAATTCCTTCGTTTCGAAATTTCTGGATTTGAAGTACCCCTTTTATCCGTTAT 480

QY 721 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATCTGTAAATTTTGGAGAAGA 780
DB 481 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATCTGTAAATTTTGGAGAAGA 540

QY 781 TTGGGATTTGACACGATTAATCTCAATGAATACTATATAGACTAATTAGGCATATTGAT 840
DB 541 TTGGGATTTGACACGATTAATCTCAATGAATACTATATAGACTAATTAGGCATATTGAT 600

QY 841 GAATATGCTGATCAGTTCGCAATACGTATATACGGGATTAATAATTTACCGAAATCT 900
DB 601 GAATATGCTGATCAGTTCGCAATACGTATATACGGGATTAATAATTTACCGAAATCT 660

QY 901 ACGTATCAAGATTTGGATATACATATATCGATTAACGAGAGACTTAACATTTGACTGATTA 960
DB 661 ACGTATCAAGATTTGGATATACATATATCGATTAACGAGAGACTTAACATTTGACTGATTA 720

QY 961 GATATCGCGCTTTCTTCCAACTATGACATAGAGATATCCAAATTCAGGCAGTTGGT 1020
DB 721 GATATCGCGCTTTCTTCCAACTATGACATAGAGATATCCAAATTCAGGCAGTTGGT 780

QY 1021 CAACTAAACAGGAGAGTTTATACGGACCCATTAATTTTAAATCCACAGTTACAGTCT 1080
DB 781 CAACTAAACAGGAGAGTTTATACGGACCCATTAATTTTAAATCCACAGTTACAGTCT 840

QY 1081 GTAGCTCAATTACCTACTTTTAAACGTTATGGAGACGCGCAATTTAGAAATCCTCATTTA 1140

DB 841 GTAGCTCAATTACCTACTTTTAAACGTTATGGAGACGCGCAATTTAGAAATCCTCATTTA 900
QY 1141 TTTGATATATTGAATAAATCTTACAAATCTTTACGGATTTGTTAGTGTGCGAGCAATTTT 1200
DB 901 TTTGATATATTGAATAAATCTTACAAATCTTTACGGATTTGTTAGTGTGCGAGCAATTTT 960
QY 1201 TATTCGGGAGGACATCGAGTAAATATCTAGCCTTTATAGGAGGTGGTAAACATAATCATCTCCT 1260
DB 961 TATTCGGGAGGACATCGAGTAAATATCTAGCCTTTATAGGAGGTGGTAAACATAATCATCTCCT 1020
QY 1261 ATATATGGAAGAGAGCGGAAACAGAGAGCTTCAAGATCTTTACTTTTAAATGGAACCGGTA 1320
DB 1021 ATATATGGAAGAGAGCGGAAACAGAGAGCTTCAAGATCTTTACTTTTAAATGGAACCGGTA 1080
QY 1321 TTTAGGACTTTATCAATTTCTACTTTTACGATTTATACGAACCTTTGCCAGCGCCACCAT 1380
DB 1081 TTTAGGACTTTATCAATTTCTACTTTTACGATTTATACGAACCTTTGCCAGCGCCACCAT 1140
QY 1381 TTTAAATTTACGTGGTGGTGAAGAGTAGAATTTTCTACACCTTACAAATAGCTTTACGTAT 1440
DB 1141 TTTAAATTTACGTGGTGGTGAAGAGTAGAATTTTCTACACCTTACAAATAGCTTTACGTAT 1200
QY 1441 GCAGGAAGAGTACCGTGTGATTTCTTAACTGAATTAACCGCTTGAGGATTAATAGTGTGCCA 1500
DB 1201 CGAGGAAGAGTACCGTGTGATTTCTTAACTGAATTAACCGCTTGAGGATTAATAGTGTGCCA 1260
QY 1501 CCTCGGAGGATATAGTCAATCTGTTATGTCATGCAACTTTTGTTCGAAGATCTGGAAACA 1560
DB 1261 CCTCGGAGGATATAGTCAATCTGTTATGTCATGCAACTTTTGTTCGAAGATCTGGAAACA 1320
QY 1561 CCTTTTAAACAATCTGTTAGTATTTTCTTGGAGCGATCGTAGTGCACCTCTTACAAAT 1620
DB 1321 CCTTTTAAACAATCTGTTAGTATTTTCTTGGAGCGATCGTAGTGCACCTCTTACAAAT 1380
QY 1621 ACATTTGATCCAGAGAGAAATTAATCAATACTTTAGTGAAGAGATTTAGTGTGGGG 1680
DB 1381 ACATTTGATCCAGAGAGAAATTAATCAATACTTTAGTGAAGAGATTTAGTGTGGGG 1440
QY 1681 GGCACCTCTGTCATTTACAGGACAGGATTTACAGGAGGGATATCCTTCGAAGAAATACC 1740
DB 1441 GGCACCTCTGTCATTTACAGGACAGGATTTACAGGAGGGATATCCTTCGAAGAAATACC 1500
QY 1741 TTTGTTGATTTTGTATCTCTCAAGTCAATATTAATTCACCAATTTACCAAGATACCGT 1800
DB 1501 TTTGTTGATTTTGTATCTCTCAAGTCAATATTAATTCACCAATTTACCAAGATACCGT 1560
QY 1801 TTAAGATTTGTTAGCTTCCAGTATAGGATGCGAGTATATAGTATTAACAGGAGCGCA 1860
DB 1561 TTAAGATTTGTTAGCTTCCAGTATAGGATGCGAGTATATAGTATTAACAGGAGCGCA 1620
QY 1861 TCCACAGAGTGGGAGGCGCAAGTTAGTGTAGATATGCTCTTCAGAAACTATGGAATA 1920
DB 1621 TCCACAGAGTGGGAGGCGCAAGTTAGTGTAGATATGCTCTTCAGAAACTATGGAATA 1680
QY 1921 GGGGAGAACTTAAACATCTAGAACATTTAGATATACCGATTTTGTAGTAACTCTTTTCATTT 1980
DB 1681 GGGGAGAACTTAAACATCTAGAACATTTAGATATACCGATTTTGTAGTAACTCTTTTCATTT 1740
QY 1981 AGAGCTAATCCAGATATTAATTTGGGATAAGTGAACAACTCTATTTTGGTGCAGGTTCTATT 2040
DB 1741 AGAGCTAATCCAGATATTAATTTGGGATAAGTGAACAACTCTATTTTGGTGCAGGTTCTATT 1800
QY 2041 AGTAGCTTGAATTTATATAGATAAATTTGAATTTTCTAGAGATGCAACATTTGAA 2100
DB 1801 AGTAGCTTGAATTTATATAGATAAATTTGAATTTTCTAGAGATGCAACATTTGAA 1860
QY 2101 GCAGAACTGTGATTTAGAAAGAGACAAAGGCGGTGAATGCCCTGTTTACTTCTTCCAAAT 2160
DB 1861 GCAGAACTGTGATTTAGAAAGAGACAAAGGCGGTGAATGCCCTGTTTACTTCTTCCAAAT 1920
QY 2161 CAAATCGGGTTAAACCGGATGTGCGGATTTATCATATTTGATCAAGTATCCAAATTTAGTG 2220

DB 1921 CAAATCGGTTAAACCGATGTGACGGATTATCATATTCATCATAGTATCAATTTAGTG 1980
QY 2221 GATTGTTTATCAGATGAATTTTCTGTGGATGAAAGCGAGATTTGTCGAGAAATCAAA 2280
DB 1981 GATTGTTTATCAGATGAATTTTCTGTGGATGAAAGCGAGATTTGTCGAGAAATCAAA 2040
QY 2281 CATGCGAAGCGACTCAGTGATGAGCGGAATTTTACCTCAAGATCAAACTTCAGAGGATC 2340
DB 2041 CATGCGAAGCGACTCAGTGATGAGCGGAATTTTACCTCAAGATCAAACTTCAGAGGATC 2100
QY 2341 AATAGACCAACGACCGTGGCTGGAGAGAGTACAGATATTACCTCAAGAGGAGAT 2400
DB 2101 AATAGACCAACGACCGTGGCTGGAGAGAGTACAGATATTACCTCAAGAGGAGAT 2160
QY 2401 GACGTATTCAAGAGAAATTACGTCACTACCGGTACCGTTGATGAGTCTTCCAAACG 2460
DB 2161 GACGTATTCAAGAGAAATTACGTCACTACCGGTACCGTTGATGAGTCTTCCAAACG 2220
QY 2461 TATTATTATCAGAAATAGATGAGTCAAAATTAAGGCTTATACCGGTTATGAATTAGA 2520
DB 2221 TATTATTATCAGAAATAGATGAGTCAAAATTAAGGCTTATACCGGTTATGAATTAGA 2280
QY 2521 CGGTATATCGAGATGACAGCTTAGAAATCTATTGATCGGTACAAATGCAAAACAC 2580
DB 2281 GGGTATATCGAGATGATGACAGCTTAGAAATCTATTGATCGGTACAAATGCAAAACAC 2340
QY 2581 GAAATAGTAATGTCCAGGACCGGTTCTTATGCGGCTTTTACGCCCTTCAGCCCAAAATGCAATC 2640
DB 2341 GAAATAGTAATGTCCAGGACCGGTTCTTATGCGGCTTTTACGCCCTTCAGCCCAAAATGCAATC 2400
QY 2641 GGAAGTGTGGAGAACCGAATGATGCGGCTTACAGCTTGAATGGAATCTGATCTAGAT 2700
DB 2401 GGAAGTGTGGAGAACCGAATGATGCGGCTTACAGCTTGAATGGAATCTGATCTAGAT 2460
QY 2701 TGTTCCTGCAG 2711
DB 2461 TGTTCCTGCAG 2471

RESULT 5
ID AAQ80646 standard; cDNA; 3567 BP.
XX AC AAQ80646;
XX DT 25-MAR-2003 (updated)
XX DT 09-OCT-1995 (first entry)
XX DE CryIC gene.
XX KW Crystal protein; toxin; insecticide; ss.
XX OS Bacillus thuringiensis sub species entomocidus 60.5.
XX PH Key Location/Qualifiers
XX FT CDS 1..3567
XX FT /*tag= a
XX PN W09506730-A1.
XX PD 09-MAR-1995.
XX PF 01-SEP-1994; 94WO-EP02909.
XX PR 02-SEP-1993; 93GB-0018207.
XX PA (SANO) SANDOZ LTD.
XX PA (SANO) SANDOZ PATENT GMBH.
XX PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX PI Bosch HJ, Stiekema WJ;
XX WPI; 1995-115446/15.
DR

DR P-PSDB; AAR71463.
XX New Bacillus thuringiensis hybrid toxin fragment - derived from
PT two different cry proteins, and related hybrid toxins,
PT recombinant DNA, vectors, transformed plants and microorganisms,
PT for insect control.
XX) Disclosure; Page 18-23; 65pp; English.
XX Crystal proteins CryIC, CryIIE and CryIYA are toxic to lepidopterans.
CC CryIC is particularly active against S. exigua and M. brassicae.
CC Toxic fragments of crystal proteins are thought to be composed of
CC three distinct structural domains. Domain I, the most N-terminal
CC domain, consists of 7 alpha-helices. Domain II comprises 3 beta-
CC sheets and domain III (the most C-terminal) folds into a beta-
CC sandwich. If projected onto CryI sequences, domain I runs from about
CC AA residue 28-260, domain II from about 260-460 and domain III from
CC about 460-600.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 3567 BP; 1168 A; 596 C; 792 G; 1011 T; 0 other;
SQ Query Match 89.7%; Score 2431; DB 16; Length 3567;
Best Local Similarity 99.0%; Pred. No. 0; Indels 0; Gaps 0;
Matches 2446; Conservative 0; Mismatches 25;
QY 241 ATGGAGGAAATATCAAAATCAATGATATCACTGATTAATCTCAATTTGATTTCTCTCA 300
DB 1 ATGGAGGAAATATCAAAATCAATGATATCACTGATTAATCTCAATTTGATTTCTCTCA 60
QY 301 GTACTTTTGGATGGAGAACCGGATATCACTGATTAATCTCAATTTGATTTCTCTCA 360
DB 61 GTACTTTTGGATGGAGAACCGGATATCACTGATTAATCTCAATTTGATTTCTCTCA 120
QY 361 CTGTGTCAGTTCTTCTGATATCACTGATTAATCTCAATTTGATTTCTCTCA 420
DB 121 CTGTGTCAGTTCTTCTGATATCACTGATTAATCTCAATTTGATTTCTCTCA 180
QY 421 GATTTTGTATGGGAAATAGTTGGCCCTTCTCAATGGGATGATTTCTAGTCAAAATTTGAA 480
DB 181 GATTTTGTATGGGAAATAGTTGGCCCTTCTCAATGGGATGATTTCTAGTCAAAATTTGAA 240
QY 481 CAATTAATTAAGAAATAGTCTGAATTTGCTAGGAATGCTGCTATTTCTTAATTTAGAA 540
DB 241 CAATTAATTAAGAAATAGTCTGAATTTGCTAGGAATGCTGCTATTTCTTAATTTAGAA 300
QY 541 GGATTTAGGAAACAAATTTCAATATATATGTGGAAGCATTTAAAGAAATGGGAAGATCCT 600
DB 301 GGATTTAGGAAACAAATTTCAATATATATGTGGAAGCATTTAAAGAAATGGGAAGATCCT 360
QY 601 AATATCCAGACACGAGGACGAGATTAATTTGATTCGCTTTCTGATATCTGATGGCTACTT 660
DB 361 AATATCCAGACACGAGGACGAGATTAATTTGATTCGCTTTCTGATATCTGATGGCTACTT 420
QY 661 GAAAGGACATTCCTTCTGATTTGGAATTTCTGATTTGGAATTTGGAATTTGGAATTTGGA 720
DB 421 GAAAGGACATTCCTTCTGATTTGGAATTTCTGATTTGGAATTTGGAATTTGGAATTTGGA 480
QY 721 GCTCAAGCGGCAATCTGCAATAGCTATTAATTAAGAGATTTCTGTAATTTTGGAGAAAGA 780
DB 481 GCTCAAGCGGCAATCTGCAATAGCTATTAATTAAGAGATTTCTGTAATTTTGGAGAAAGA 540
QY 781 TTGGATTTGACAAACGATTAATGTCATTAAGAACTTAATTAAGAACTTAATTAAGAACTTAAT 840
DB 541 TTGGATTTGACAAACGATTAATGTCATTAAGAACTTAATTAAGAACTTAATTAAGAACTTAAT 600
QY 841 GAATATGCTGATCACTGTCGCAATACGATTAATTAAGAACTTAATTAAGAACTTAATTAAGAACT 900
DB 601 GAATATGCTGATCACTGTCGCAATACGATTAATTAAGAACTTAATTAAGAACTTAATTAAGAACT 660
QY 901 ACGTATCAAGATTGGATAACATTAATTCGATTTACGAGAGACTTAAGAACTTAAGAACTTAATTA 960
DB 661 ACGTATCAAGATTGGATAACATTAATTCGATTTACGAGAGACTTAAGAACTTAAGAACTTAATTA 720

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QY 961 GATATGCGCGCTTTCTTTCCAACTATGACAATAGAGAGATATCAATTCAGCCAGTTGGT 1020
DB 721 GATATGCGCGCTTTCTTTCCAACTATGACAATAGAGAGATATCAATTCAGCCAGTTGGT 780
QY 1021 CAATTAACAGGGAAGTTTATACGGACCCCAATTAATTAATTTTAAATCCACAGTTACAGTCT 1080
DB 781 CAATTAACAGGGAAGTTTATACGGACCCCAATTAATTAATTTTAAATCCACAGTTACAGTCT 840
QY 1081 GTAGCTCAATTAACCTACTTTTAACTGTTATGGAGAGAGCGCAATTAAGAAATCCCTCATTTA 1140
DB 841 GTAGCTCAATTAACCTACTTTTAACTGTTATGGAGAGAGCGCAATTAAGAAATCCCTCATTTA 900
QY 1141 TTTGATATATGAATTAATCTTAACAATCTTTACCGATTTGGTTAGTGTGGACGCAATTTT 1200
DB 901 TTTGATATATGAATTAATCTTAACAATCTTTACCGATTTGGTTAGTGTGGACGCAATTTT 960
QY 1201 TATTGGGAGGACATCGAGTAATATCTAGCCTTTATAGGAGGTGTTAACATAATCTCCT 1260
DB 961 TATTGGGAGGACATCGAGTAATATCTAGCCTTTATAGGAGGTGTTAACATAATCTCCT 1020
QY 1261 ATATATGGAAGAGAGCGCAACAGGAGCCTTCCAGATCTTTACTTTTAAATGACCGGTA 1320
DB 1021 ATATATGGAAGAGAGCGCAACAGGAGCCTTCCAGATCTTTACTTTTAAATGACCGGTA 1080
QY 1321 TTTAGGACTTTATCAAAATCTTACTTTACGATTAATACAGCAACTTTGGCGAGCGCACCA 1380
DB 1081 TTTAGGACTTTATCAAAATCTTACTTTACGATTAATACAGCAACTTTGGCGAGCGCACCA 1140
QY 1381 TTTAAATTTACGTCGTCGAGGAGTAGAATTTCTTACACCTAACAATAGCTTTACGTAT 1440
DB 1141 TTTAAATTTACGTCGTCGAGGAGTAGAATTTCTTACACCTAACAATAGCTTTACGTAT 1200
QY 1441 GCAGGAAGAGGTACGGTTGATCTTTAACTGAATTAACCGCTCAGGATTAATAGTGTGCCA 1500
DB 1201 CGAGGAAGAGGTACGGTTGATCTTTAACTGAATTAACCGCTCAGGATTAATAGTGTGCCA 1260
QY 1501 CCTCGGAAGGATATAGTCAATCTTTATGTCATGCAACTTTTGTTCAGAGATCTGGAACA 1560
DB 1261 CCTCGGAAGGATATAGTCAATCTTTATGTCATGCAACTTTTGTTCAGAGATCTGGAACA 1320
QY 1561 CCTTTTAACTACACTCGGTAGTATTTTCTTGACGCAATCGTAGTCAACTCTTACAAT 1620
DB 1321 CCTTTTAACTACACTCGGTAGTATTTTCTTGACGCAATCGTAGTCAACTCTTACAAT 1380
QY 1621 ACAATTTGATCCAGAGAGAATTAATCAAAATACCTTTAGTGAAGGATTTAGAGTTTCGGG 1680
DB 1381 ACAATTTGATCCAGAGAGAATTAATCAAAATACCTTTAGTGAAGGATTTAGAGTTTCGGG 1440
QY 1681 GGCACCTCTGTCTATACAGGACCAAGATTTACAGGAGGGGATATCTTCCGAGAAATACC 1740
DB 1441 GGCACCTCTGTCTATACAGGACCAAGATTTACAGGAGGGGATATCTTCCGAGAAATACC 1500
QY 1741 TTTGGTGAATTTGTATCTCTACAGTCAATTAATTAATTCACCAATTAACCAAGATACCGT 1800
DB 1501 TTTGGTGAATTTGTATCTCTACAGTCAATTAATTAATTCACCAATTAACCAAGATACCGT 1560
QY 1801 TTAAGATTTTCGTTACCGCTTCCAGTAGGATGACAGAGTTATAGTATTAACAGAGCGGCA 1860
DB 1561 TTAAGATTTTCGTTACCGCTTCCAGTAGGATGACAGAGTTATAGTATTAACAGAGCGGCA 1620
QY 1861 TCCACAGGAGTGGGAGGCGCAAGTTAGTGTAGATATGCTCTTCCAGAAATCTATGGAATA 1920
DB 1621 TCCACAGGAGTGGGAGGCGCAAGTTAGTGTAGATATGCTCTTCCAGAAATCTATGGAATA 1680
QY 1921 GGGGAGAACTTAACATCTAGAACATTTAGATATACCGATTTAGTAAATCTTTTCAATTT 1980
DB 1681 GGGGAGAACTTAACATCTAGAACATTTAGATATACCGATTTAGTAAATCTTTTCAATTT 1740
QY 1981 AGAGCTTAATCCAGATATAATTTGGATAAGTGAACACCTCTATTTGTCGACGCTTCTATT 2040
DB 1741 AGAGCTTAATCCAGATATAATTTGGATAAGTGAACACACCTCTATTTTGGTCAGGCTTCTATT 1800
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QY 2041 AGTAGCGTTGAACCTTTATATATAGATAAAATTTGAAATTTATTTCTAGCAGATGCAACATTTGAA 2100
DB 1801 AGTAGCGTTGAACCTTTATATATAGATAAAATTTGAAATTTATTTCTAGCAGATGCAACATTTGAA 1860
QY 2101 GCAGATCTGATTTAGAAAGAGCACAAGAGCGGTCGAATGCGCTGTTACTTCTTCCAAT 2160
DB 1861 GCAGATCTGATTTAGAAAGAGCACAAGAGCGGTCGAATGCGCTGTTACTTCTTCCAAT 1920
QY 2161 CAAATCGGTTAAAAACCGATGTGACGGATTTATCATATTTGATCAAGTATCCATTTTAGTG 2220
DB 1921 CAAATCGGTTAAAAACCGATGTGACGGATTTATCATATTTGATCAAGTATCCATTTTAGTG 1980
QY 2221 GATTTGTTATCAGATGAATTTTGTCTGATGAAAGCGGAAATTTGTCGAGAGAAAGTCAAA 2280
DB 1981 GATTTGTTATCAGATGAATTTTGTCTGATGAAAGCGGAAATTTGTCGAGAGAAAGTCAAA 2040
QY 2281 CATGCGAAGCGACTCAGTCAATGAGCGGAAATTTACTTTCAAGATCCAACTTCAGAGGGATC 2340
DB 2041 CATGCGAAGCGACTCAGTCAATGAGCGGAAATTTACTTTCAAGATCCAACTTCAGAGGGATC 2100
QY 2341 AATAGACAACAGACCGTGGCTGGAGAGGAAGTACAGATATTTACCATCCAAGGAGGAT 2400
DB 2101 AATAGACAACAGACCGTGGCTGGAGAGGAAGTACAGATATTTACCATCCAAGGAGGAT 2160
QY 2401 GACGTATTTCAAGAGAAATTAACGTCACTACCGGGTACCGTTGATGAGTCTATCCAACG 2460
DB 2161 GACGTATTTCAAGAGAAATTAACGTCACTACCGGGTACCGTTGATGAGTCTATCCAACG 2220
QY 2461 TATTATATACAGAAATAGATGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 2520
DB 2221 TATTATATACAGAAATAGATGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 2280
QY 2521 GGGTATATCGAAGATAGTCAAGATTTAGAAATCTATTTGATCGGTACCAATGCAAAACAC 2580
DB 2281 GGGTATATCGAAGATAGTCAAGATTTAGAAATCTATTTGATCGGTACCAATGCAAAACAC 2340
QY 2581 GAAATAGTAAATGTGCCAGGCAAGGTTCCCTTATGCGCGCTTTACGCCAAAGTCCAATC 2640
DB 2341 GAAATAGTAAATGTGCCAGGCAAGGTTCCCTTATGCGCGCTTTACGCCAAAGTCCAATC 2400
QY 2641 GGAAGTGTGGAGAACCGAATCGATGCGCGCCACACCTTTGAATGGAATCCTGATCTAGAT 2700
DB 2401 GGAAGTGTGGAGAACCGAATCGATGCGCGCCACACCTTTGAATGGAATCCTGATCTAGAT 2460
QY 2701 TGTCTCTGCG 2711
DB 2461 TGTCTCTGCG 2471

RESULT 6
AAQ47294
ID AAQ47294 standard; DNA; 3567 BP.
XX
AC AAQ47294;
XX
DT 25-MAR-2003 (updated)
DT 28-JAN-1994 (first entry)
XX
DE Delta endotoxin gene.
XX
KW Endotoxin; Bacillus; lice; insecticide; sheep; ss.
XX
OS Bacillus thuringiensis PS811 (Clone B2).
XX
FH Key Location/Qualifiers
FT mat_peptide 1..3567
FT /tag= a
FT /product= delta endotoxin.
XX
PN WO9314641-Al.
XX
PD 05-AUG-1993.
XX
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Db 1681 GGGGAGAACTTAACATCTAGAACATTTAGATATACCGATTTTAGTAATCTCTTTTCAATTT 1740

QY 1981 AGAGCTAAATCCAGATATAATTTGGGATAAGTGAACAACCTCTATTCTTGGTGCAGGTTCTATT 2040

Db 1741 AGAGCTAAATCCAGATATAATTTGGGATAAGTGAACAACCTCTATTCTTGGTGCAGGTTCTATT 1800

QY 2041 AGTAGGTTGAACCTTTATATAGATAAAATTTGAAATTTATTTCTAGCAGATGCAACATTTGAA 2100

Db 1801 AGTAGGCGGTGAACCTTTATATAGATAAAATTTGAAATTTATTTCTAGCAGATGCAACATTTGAA 1860

QY 2101 GCAGAACTCTGATTTAGAAAGAGACAAAGGCGGTGAATGCGCTGTTTACTTCTTCCCAAT 2160

Db 1861 GCAGAACTCTGATTTAGAAAGAGACAAAGGCGGTGAATGCGCTGTTTACTTCTTCCCAAT 1920

QY 2161 CAAATCGGTTAAAAACCGATGTGACGGAATTAATCATATTGATCAAGTATCCCAATTTAGTG 2220

Db 1921 CAAATCGGTTAAAAACCGATGTGACGGAATTAATCATATTGATCAAGTATCCCAATTTAGTG 1980

QY 2221 GATTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGGAGAAATTTGTCGAGAAAGTCAAA 2280

Db 1981 GATTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGGAGAAATTTGTCGAGAAAGTCAAA 2040

QY 2281 CATGCGAAGCGACTCAGTGTGATGAGCGGAATTTTACTTCAAGATCCAAACTTTCAGAGGGATC 2340

Db 2041 CATGCGAAGCGACTCAGTGTGATGAGCGGAATTTTACTTCAAGATCCAAACTTTCAGAGGGATC 2100

QY 2341 AATAGACAACACGACCGTGGCTGGAGAGGAAGTACAGATATTACCATCCAAGGAGGAGAT 2400

Db 2101 AATAGACAACACGACCGTGGCTGGAGAGGAAGTACAGATATTACCATCCAAGGAGGAGAT 2160

QY 2401 GAGTATTCAGAGAAATTAACGTCACACTACCGGGTACCGTTGATGAGTGCTATCCAACG 2460

Db 2161 GAGTATTCAGAGAAATTAACGTCACACTACCGGGTACCGTTGATGAGTGCTATCCAACG 2220

QY 2461 TATTTATATCAGAAATAGATGAGTGGAAATTTAAAGCTTATACCGTTATGAAATTAAGA 2520

Db 2221 TATTTATATCAGAAATAGATGAGTGGAAATTTAAAGCTTATACCGTTATGAAATTAAGA 2280

QY 2521 GGGTATATCGAAGATAGTCAAGACTTAGAAATCTATTGATCGGTCGATCAAGTCAAAACAC 2580

Db 2281 GGGTATATCGAAGATAGTCAAGACTTAGAAATCTATTGATCGGTCGATCAAGTCAAAACAC 2340

QY 2581 GAAATAGTAAATGTGCCAGCAGCGGTTCTTATGCGCTTTTACGCCCAAAAGTCCAATC 2640

Db 2341 GAAATAGTAAATGTGCCAGCAGCGGTTCTTATGCGCTTTTACGCCCAAAAGTCCAATC 2400

QY 2641 GGAAGTGTGGAAACCGAATCGATGCGGCCACACCTTGAATGGAATCTGATCTAGAT 2700

Db 2401 GGAAGTGTGGAAACCGAATCGATGCGGCCACACCTTGAATGGAATCTGATCTAGAT 2460

QY 2701 TGTTCCTGCAG 2711

Db 2461 TGTTCCTGCAG 2471

RESULT 7

AAV27848

ID AAV27848 standard; DNA; 3567 BP.

XX AC

AAV27848;

XX DT

30-SEP-1998 (first entry)

XX DE

DNA encoding a mutated CryIC protein designated CryIC.499.

XX KW

Mutant; CryIC delta-endotoxin; CryIC.579; insecticidal activity;

KW control; insect; Lepidoptera; Spodoptera exigua; Plutella xylostella;

XX KW

Trichoplusia ni; Spodoptera frugiperda; ss.

XX OS

Synthetic.

OS Bacillus thuringiensis.

XX FH

Key Location/Qualifiers

CDS

FT FT 1..3567

FT FT /tag= a

FT FT /note= "no stop codon given"

mutation

360

/tag= a

/note= "T changed to C"

361

/tag= b

/note= "A changed to C"

XX

W09823641-A1.

PN

XX

04-JUN-1998.

XX

26-NOV-1997;

97WO-US22181.

XX

27-NOV-1996;

96US-0757536.

XX

(ECOG-) ECOGEN INC.

XX

Baum JA, Gilmer AJ, Mettuss A;

XX

WPI; 1998-322660/28.

DR

P-PSDB; AAW61340.

XX

New Bacillus thuringiensis nucleic acid segments - comprising

PT

delta-endotoxin gene fragments, used for the control of insects,

PT

particularly Lepidopteran pests

XX

Claim 4; Pages 130-131; 270pp; English.

PS

XX

The present sequence encodes a mutant of the CryIC delta-endotoxin

CC

of Bacillus thuringiensis designated CryIC.499, where the Asn at

CC

position 121 of the wild type CryIC protein is substituted with His.

CC

The protein shows insecticidal activity, and can be sprayed onto

CC

plants or expressed in transgenic plants for the control of insects,

CC

particularly Lepidopteran pests such as Spodoptera exigua, Plutella

CC

xylostella, Trichoplusia ni and Spodoptera frugiperda.

XX

Sequence 3567 BP; 1167 A; 599 C; 791 G; 1010 T; 0 other;

SQ

Query Match

Best Local Similarity

Matches 2445; Conservative

Mismatches 26; Indels 0; Gaps 0;

Score 2429.4; DB 19; Length 3567;

Pred. No. 0;

0; Mismatches 26; Indels 0; Gaps 0;

0; Mismatches 26; Indels 0; Gaps 0;

0; Mismatches 26; Indels 0; Gaps 0;

0; Mismatches 26; Indels 0; Gaps 0;

0; Mismatches 26; Indels 0; Gaps 0;

0; Mismatches 26; Indels 0; Gaps 0;

0; Mismatches 26; Indels 0; Gaps 0;

0; Mismatches 26; Indels 0; Gaps 0;

0; Mismatches 26; Indels 0; Gaps 0;

0; Mismatches 26; Indels 0; Gaps 0;

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0; Mismatches 26; Indels 0; Gaps 0;

0; Mismatches 26; Indels 0; Gaps 0;

0; Mismatches 26; Indels 0; Gaps 0;

0; Mismatches 26; Indels 0; Gaps 0;

Qy 661 GAAAGGACATCTCTTCGTTTCTGAAATCTTCGATTTGAAGTACCCCTTTTATCCGTTTAT 720
Db |||||
Qy 421 GAAAGGACATCTCTTCGTTTCTGAAATCTTCGATTTGAAGTACCCCTTTTATCCGTTTAT 480
Db |||||
Qy 721 GCTCAAGCGCCCAATCTGCATCTAGCTATTAATTAAGAGATCTCTTAATTTTTCGGAAGA 780
Db |||||
Qy 481 GCTCAAGCGCCCAATCTGCATCTAGCTATTAATTAAGAGATCTCTTAATTTTTCGGAAGA 540
Db |||||
Qy 781 TTGGGATGCAACAGATTAATGTCATGAAACTATTAATTAAGATCTTAATTTAGGCAATTTAT 840
Db |||||
Qy 541 TTGGGATGCAACAGATTAATGTCATGAAACTATTAATTAAGATCTTAATTTAGGCAATTTAT 600
Db |||||
Qy 841 GAATATCTCATCTCTGTCGAAATATCGTATATCTGCGGATTTAAATTAATTTACGGAATCT 900
Db |||||
Qy 601 GAATATCTCATCTCTGTCGAAATATCGTATATCTGCGGATTTAAATTAATTTACGGAATCT 660
Db |||||
Qy 901 ACCTATCAAGATTTGGATTAACATATAATCGATTAACGAGAGACTTAACATTTGACTGTATTA 960
Db |||||
Qy 661 ACCTATCAAGATTTGGATTAACATATAATCGATTAACGAGAGACTTAACATTTGACTGTATTA 720
Db |||||
Qy 961 GATATCTCGCTCTTTCTTTCCAACTATGACAAATAGAGATATCCAAATTCAGCGAGTTGGT 1020
Db |||||
Qy 721 GATATCTCGCTCTTTCTTTCCAACTATGACAAATAGAGATATCCAAATTCAGCGAGTTGGT 780
Db |||||
Qy 1021 CAACTTAACAGGGAAGTTTATACGAGCCCAATTAATTAATTTTAAATCCACAGTTACAGTCT 1080
Db |||||
Qy 781 CAACTTAACAGGGAAGTTTATACGAGCCCAATTAATTAATTTTAAATCCACAGTTACAGTCT 840
Db |||||
Qy 1081 GTAGTCAATTTACTTCTTTTAAAGTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db |||||
Qy 841 GTAGTCAATTTACTTCTTTTAAAGTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db |||||
Qy 1141 TTTGATATATTGAATAATCTTACCAATCTTTACGATTTGGTTTGGTGGAGCCCAATTTT 1200
Db |||||
Qy 901 TTTGATATATTGAATAATCTTACCAATCTTTACGATTTGGTTTGGTGGAGCCCAATTTT 960
Db |||||
Qy 1201 TATTGGGAGGACATCGAGTATATCTAGCTTATAGAGAGTGGTAAACATATCTCT 1260
Db |||||
Qy 961 TATTGGGAGGACATCGAGTATATCTAGCTTATAGAGAGTGGTAAACATATCTCT 1020
Db |||||
Qy 1261 ATATATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
Db |||||
Qy 1021 ATATATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
Db |||||
Qy 1321 TTTAGGACTTTATCAATCTCTACTTTTACGATTTATACGACACCTTGCAGCGCCACCAT 1380
Db |||||
Qy 1081 TTTAGGACTTTATCAATCTCTACTTTTACGATTTATACGACACCTTGCAGCGCCACCAT 1140
Db |||||
Qy 1381 TTTAATTTACGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
Db |||||
Qy 1141 TTTAATTTACGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
Db |||||
Qy 1441 GCAGGAGAGGTACGGTTGATTTCTTAATCTGATTAACGCTGAGGATTAATAGTGCCCA 1500
Db |||||
Qy 1201 CGAGGAGAGGTACGGTTGATTTCTTAATCTGATTAACGCTGAGGATTAATAGTGCCCA 1260
Db |||||
Qy 1501 CTTCCGGAAGGATATAGTCAATCGTTTATGTCAATGCAATTTTGTTCGAAGATCTGGAACA 1560
Db |||||
Qy 1261 CTTCCGGAAGGATATAGTCAATCGTTTATGTCAATGCAATTTTGTTCGAAGATCTGGAACA 1320
Db |||||
Qy 1561 CTTTTTTTAACTGCTGTAGTATTTTCTTGGAGCATCTGAGTGCAATCTTTTACAAT 1620
Db |||||
Qy 1321 CTTTTTTTAACTGCTGTAGTATTTCTTGGAGCATCTGAGTGCAATCTTTTACAAT 1380
Db |||||
Qy 1621 ACAATTTGATCCAGAGAGAAATTAATCAATATCTTTAGTGAAGGATTTAGAGTTTGGGG 1680
Db |||||
Qy 1381 ACAATTTGATCCAGAGAGAAATTAATCAATATCTTTAGTGAAGGATTTAGAGTTTGGGG 1440
Db |||||
Qy 1681 GGCACCTCTGTCAATTAACAGGAGGAGGATTTACAGGAGGAGGATATCTTTCGAAGAAATACC 1740
Db |||||
Qy 1441 GGCACCTCTGTCAATTAACAGGAGGAGGATTTACAGGAGGAGGATATCTTTCGAAGAAATACC 1500
Db |||||
Qy 1741 TTTGGTGAATTTTGTATCTCTCAAGTCAATATTAATTCACCAATTAACCAAGATACCGT 1800

RESULT 8

AAV27843

ID AAV27843 standard; DNA; 3567 BP.

XX

AC AAV27843;

Db 1501 TTTGGTGAATTTTGTATCTCTACAGTCAATATTAATTCACCAATTAACCAAGATACCGT 1560
Qy |||||
Db 1801 TTAAGATTTTCGTTTACGCTTCCAGTAGGATGACAGAGTTATAGTATTAACAGGAGCGCA 1860
Qy |||||
Db 1561 TTAAGATTTTCGTTTACGCTTCCAGTAGGATGACAGAGTTATAGTATTAACAGGAGCGCA 1620
Qy |||||
Db 1861 TCCACAGGAGTGGGAGGCGCAAGTTAGTGTAGATATGCTCTTTCAGAAAACTATGGAATA 1920
Db |||||
Db 1621 TCCACAGGAGTGGGAGGCGCAAGTTAGTGTAAATATGCTCTTTCAGAAAACTATGGAATA 1680
Qy |||||
Qy 1921 GGGGAGAACTTAACATCTAGAACTTTAGATATACCGATTTTAGTAAATCTTTTTCATTT 1980
Db |||||
Db 1681 GGGGAGAACTTAACATCTAGAACTTTAGATATACCGATTTTAGTAAATCTTTTTCATTT 1740
Qy |||||
Qy 1981 AGAGCTAAATCCAGATATAATTTGGGATAAGTGAACAACTCTATTTTGGTGCAGGTTCTATT 2040
Db |||||
Db 1741 AGAGCTAAATCCAGATATAATTTGGGATAAGTGAACAACTCTATTTTGGTGCAGGTTCTATT 1800
Qy |||||
Qy 2041 AGTAGCGTTTGAACCTTTATATAGATTAATTTGAAATTTATTTCTAGCAGATGCAACATTTGAA 2100
Db |||||
Db 1801 AGTAGCGTTTGAACCTTTATATAGATTAATTTGAAATTTATTTCTAGCAGATGCAACATTTGAA 1860
Qy |||||
Qy 2101 GCAGATCTGATTTAGAAAGGACACAAAGGCGGTGAATGCCCTGTTTACTTTTCTTCCAAAT 2160
Db |||||
Db 1861 GCAGATCTGATTTAGAAAGGACACAAAGGCGGTGAATGCCCTGTTTACTTTTCTTCCAAAT 1920
Qy |||||
Qy 2161 CAAATCGGGTTAAAACCGATGTGACGGATTTATCATTTGATCAAGTATCCAAATTTAGTG 2220
Db |||||
Db 1921 CAAATCGGGTTAAAACCGATGTGACGGATTTATCATTTGATCAAGTATCCAAATTTAGTG 1980
Qy |||||
Qy 2221 GATTTGTTATCAGATGAATTTTGTCTGGATGAAGGAGAAATTTGTCGAGAAAGTCAAA 2280
Db |||||
Db 1981 GATTTGTTATCAGATGAATTTTGTCTGGATGAAGGAGAAATTTGTCGAGAAAGTCAAA 2040
Qy |||||
Qy 2281 CATCGAAGCGACTCAGTGATGAGCGGAATTTTCTTCAAGATCCAACTTTCAGAGGATC 2340
Db |||||
Db 2041 CATCGAAGCGACTCAGTGATGAGCGGAATTTTCTTCAAGATCCAACTTTCAGAGGATC 2100
Qy |||||
Qy 2341 AATAGACACACAGACCGCTGGCTGGAGAGGAGTACAGATATATACCATCCAAAGAGAGAT 2400
Db |||||
Db 2101 AATAGACACACAGACCGCTGGCTGGAGAGGAGTACAGATATATACCATCCAAAGAGAGAT 2160
Qy |||||
Qy 2401 GACGTATTTCAAAGAGAAATTAACGTCACTACCGGGTACCGTTGATGAGTGCTATCCAAAG 2460
Db |||||
Db 2161 GACGTATTTCAAAGAGAAATTAACGTCACTACCGGGTACCGTTGATGAGTGCTATCCAAAG 2220
Qy |||||
Qy 2461 TATTTATATCAGAAAAATAGATGAGTCCGAAATTTAAAAGCTTATACCCGTTATGAATTAAGA 2520
Db |||||
Db 2221 TATTTATATCAGAAAAATAGATGAGTCCGAAATTTAAAAGCTTATACCCGTTATGAATTAAGA 2280
Qy |||||
Qy 2521 GGGTATATCAGAAATAGTCAAGACTTAGAAATCTATTTGATCGGTTACAAATGCAAAACAC 2580
Db |||||
Db 2281 GGGTATATCAGAAATAGTCAAGACTTAGAAATCTATTTGATCCGTTTACAAATGCAAAACAC 2340
Qy |||||
Db 2581 GAAATAGTAAATGTCAGGACCGGTTTCTTATGCGGCTTTCAGGCCAAAGTCCCAATC 2640
Db |||||
Db 2341 GAAATAGTAAATGTCAGGACCGGTTTCTTATGCGGCTTTCAGGCCAAAGTCCCAATC 2400
Qy |||||
Qy 2641 GGAAGTGTGAGAACCGGATGAGTGGCGCCACACTTTGAATGGAATCTCTGATCTAGAT 2700
Db |||||
Db 2401 GGAAGTGTGAGAACCGGATGAGTGGCGCCACACTTTGAATGGAATCTCTGATCTAGAT 2460
Qy |||||
Qy 2701 TGTTCCTGCGAG 2711
Db |||||
Db 2461 TGTTCCTGCGAG 2471

RESULT 8

AAV27843

ID AAV27843 standard; DNA; 3567 BP.

XX

AC AAV27843;

XX 30-SEP-1998 (first entry)
 XX DNA encoding a mutated Cry1C protein designated Cry1C-R148A.
 XX Mutant; Cry1C delta-endotoxin; Cry1C-R148A; insecticidal activity;
 KW control; insect; Lepidoptera; Spodoptera exigua; Plutella xylostella;
 KW Trichoplusia ni; Spodoptera frugiperda; ss.
 XX Synthetic.
 OS Bacillus thuringiensis.
 XX Location/Qualifiers
 FH 1..3567
 FT CDS
 FT /*tag= a
 FT /note= "no stop codon given"
 XX
 XX W09823641-A1.
 XX
 XX 04-JUN-1998.
 XX
 XX 26-NOV-1997; 97WO-US22181.
 XX
 XX 27-NOV-1996; 96US-0757536.
 XX
 XX (ECOG-) ECOGEN INC.
 XX
 XX Baum JA, Gilmer AJ, Mettus A;
 XX WPI: 1998-322660/28.
 XX P-PSDB; AAM61335.
 XX
 XX New Bacillus thuringiensis nucleic acid segments - comprising
 PT delta-endotoxin gene fragments, used for the control of insects,
 PT particularly Lepidopteran pests
 XX
 XX Claim 4; Pages 126-127; 270pp; English.
 XX
 XX The present sequence encodes a mutant of the Cry1C delta-endotoxin
 CC of Bacillus thuringiensis designated Cry1C-R148A. The protein shows
 CC insecticidal activity, and can be sprayed onto plants or expressed in
 CC transgenic plants for the control of insects, particularly Lepidopteran
 CC pests such as Spodoptera exigua, Plutella xylostella, Trichoplusia ni
 CC and Spodoptera frugiperda.
 XX
 XX Sequence 3567 BP; 1168 A; 597 C; 791 G; 1011 T; 0 other;
 SQ

Query Match 89.6%; Score 2429.4; DB 19; Length 3567;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 241 ATGGAGGAAATAATCAAAATCAATGCATACCTTACAAATGTTTAAAGTAATCCTGAAGAA 300
 DB 1 ATGGAGGAAATAATCAAAATCAATGCATACCTTACAAATGTTTAAAGTAATCCTGAAGAA 60
 QY 301 GTCATTTGGATGGAGAACGGATATCAACTGGTAATTAATCAATTCATATTTCTCTGTCA 360
 DB 61 GTCATTTGGATGGAGAACGGATATCAACTGGTAATTCATCAATTCATATTTCTCTGTCA 120
 QY 361 CTTGTTTCAGTTTCTGGTATCACTTTGTACAGGGGGAGGATTTTATGTTGGATTAATA 420
 DB 121 CTTGTTTCAGTTTCTGGTATCACTTTGTACAGGGGGAGGATTTTATGTTGGATTAATA 180
 QY 421 GATTTTGTATGGGAATAGTTCGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTCGA 480
 DB 181 GATTTTGTATGGGAATAGTTCGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTCGA 240
 QY 481 CAATTAATTAATGAAGAATAGTTCGAATTTGTAGGAATGCTGCTATTGCTTAATTTAGAA 540
 DB 241 CAATTAATTAATGAAGAATAGTTCGAATTTGTAGGAATGCTGCTATTGCTTAATTTAGAA 300
 QY 541 GGATTAGGAACAATTTCAATATATATGTGGAAGCATTTAAAGAAATGGGAAGAGATCCT 600

DB 301 GGATTAGGAACAATTTCAATATATATGTGGAAGCATTTAAAGAAATGGGAAGAGATCCT 360
 QY 601 AATAATCCAGCAACCCAGGACCCAGAGTAATATGATCCCTTTTCGTATATCTTGTATGATGGGTACTTT 660
 DB 361 AATAATCCAGCAACCCAGGACCCAGAGTAATATGATCCCTTTTCGTATATCTTGTATGATGGGTACTTT 420
 QY 661 GAAAGGACATTTCTTCGTTTCGTAATTTCTGGATTTGAAGTACCCTTTTATCCGTTTAT 720
 DB 421 GAAAGGACATTTCTTCGTTTCGTAATTTCTGGATTTGAAGTACCCTTTTATCCGTTTAT 480
 QY 721 GCTCAAGGGCCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTTCGAGAGAAGA 780
 DB 481 GCTCAAGGGCCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTTCGAGAGAAGA 540
 QY 781 TTGGGATTTGCAACAACGATAAATGTCAATGAAACTATAATAGACTAATTAGGCATATTGAT 840
 DB 541 TGGGGATTTGCAACAACGATAAATGTCAATGAAACTATAATAGACTAATTAGGCATATTGAT 600
 QY 841 GAATATGCTGATCACTGTGCAAAATACGTATTAATCGGGGATTAAATAATTTTACCGAAATCT 900
 DB 601 GAATATGCTGATCACTGTGCAAAATACGTATTAATCGGGGATTAAATAATTTTACCGAAATCT 660
 QY 901 ACGTATCAAGATTTGGAATAACATATATCGATTAATCGGAGAGACTTAACATTGACTGTATTA 960
 DB 661 ACGTATCAAGATTTGGAATAACATATATCGATTAATCGGAGAGACTTAACATTGACTGTATTA 720
 QY 961 GATATCGCGCGCTTTCTTTCCAAACTATGACAAATAGAGATATCCAAATTCAGCCAGTTGCT 1020
 DB 721 GATATCGCGCGCTTTCTTTCCAAACTATGACAAATAGAGATATCCAAATTCAGCCAGTTGCT 780
 QY 1021 CAACTAACAGGGGAAGTTTATACGGACCCATTAATTAATTTTAAATCCACAGTTTACAGTCT 1080
 DB 781 CAACTAACAGGGGAAGTTTATACGGACCCATTAATTAATTTTAAATCCACAGTTTACAGTCT 840
 QY 1081 GTAGCTCAATTTACCTACTTTTAAAGTTATGAGAGACAGCGCAATTAGAAAATCCTCATTTA 1140
 DB 841 GTAGCTCAATTTACCTACTTTTAAAGTTATGAGAGACAGCGCAATTAGAAAATCCTCATTTA 900
 QY 1141 TTTGATATATTGAATAATCTTACAACTTTTACGGAATGCTTTAGTGTGGAGCAATTTT 1200
 DB 901 TTTGATATATTGAATAATCTTACAACTTTTACGGAATGCTTTAGTGTGGAGCAATTTT 960
 QY 1201 TATTGGGAGGACATCGAGTAATATCTAGCCCTTATAGGAGGTGGTAAACATCAATCTCTCT 1260
 DB 961 TATTGGGAGGACATCGAGTAATATCTAGCCCTTATAGGAGGTGGTAAACATCAATCTCTCT 1020
 QY 1261 ATATATGGAAGAGAGCGCAACAGAGGCTTCAAGATCCTTTTAAATGAGACCGGTA 1320
 DB 1021 ATATATGGAAGAGAGCGCAACAGAGGCTTCAAGATCCTTTTAAATGAGACCGGTA 1080
 QY 1321 TTTAGGACTTTTATCAATTTCTTACGATTTTACAGCAACCTTTCAGCGGCCACCAT 1380
 DB 1081 TTTAGGACTTTTATCAATTTCTTACGATTTTACAGCAACCTTTCAGCGGCCACCAT 1140
 QY 1381 TTTAATTTACGTTGGTGAAGAGTAGAATTTTCTACACCTTACAAATAGCTTTTACGTAAT 1440
 DB 1141 TTTAATTTACGTTGGTGAAGAGTAGAATTTTCTACACCTTACAAATAGCTTTTACGTAAT 1200
 QY 1441 GCAGGAAGAGGTACGGTTGATTTCTTAACTGAAATTAACGCGCTGAGGATAAATAGTGTGCA 1500
 DB 1201 CGAGGAAGAGGTACGGTTGATTTCTTAACTGAAATTAACGCGCTGAGGATAAATAGTGTGCA 1260
 QY 1501 CCTCGGAAGGATATAGTTCATCGTTTATGTCATCACTTTTGTTCGAAGATCTGGAACA 1560
 DB 1261 CCTCGGAAGGATATAGTTCATCGTTTATGTCATCACTTTTGTTCGAAGATCTGGAACA 1320
 QY 1561 CCTTTTAAACAACTGGGTAGTATTTTCTTGGAGCGATTCGTAGTGCACCTCTTACAAT 1620
 DB 1321 CCTTTTAAACAACTGGGTAGTATTTTCTTGGAGCGATTCGTAGTGCACCTCTTACAAT 1380
 QY 1621 ACAATTTGATCCAGAGAGAAATTAATCAATACCTTTTGTGAAAGGATTTAGAGTTTGGGG 1680
 DB 1381 ACAATTTGATCCAGAGAGAAATTAATCAATACCTTTTGTGAAAGGATTTAGAGTTTGGGG 1440

[illegible]

QY 421 GATTTTGTATGGGAATAGTTGGCCCTTCTCAATGGGATGCATTTCTAGTACAAATTGAA 480
DB 181 GATTTTGTATGGGAATAGTTGGCCCTTCTCAATGGGATGCATTTCTAGTACAAATTGAA 240
QY 481 CAATTAATTAATGAAAGAAATAGCTGAATTTGCTAGGAATGCTGCTAATTCCTAATTTAGAA 540
DB 241 CAATTAATTAATGAAAGAAATAGCTGAATTTGCTAGGAATGCTGCTAATTCCTAATTTAGAA 300
QY 541 GGATTAAGGAACAAATTTCAATATATATGTGGAGCAATTTAAAGAAATGGGAAGAAATCCT 600
DB 301 GGATTAAGGAACAAATTTCAATATATATGTGGAGCAATTTAAAGAAATGGGAAGAAATCCT 360
QY 601 AATAATCCAGACACAGGACAGGATTAATGTATGCTGCTTTCTGATACCTGATGGCTACTT 660
DB 361 CATAAATCCAGCAACCAAGGACCAAGTAATGTATGCTGCTTTCTGATACCTGATGGCTACTT 420
QY 661 GAAAGGACATTTCTGCTTTGCAATTTCTGGATTTGAAGTACCCCTTTTATCCGTTTAT 720
DB 421 GAAAGGACATTTCTGCTTTGCAATTTCTGGATTTGAAGTACCCCTTTTATCCGTTTAT 480
QY 721 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTGGAGAAAGA 780
DB 481 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTGGAGAAAGA 540
QY 781 TTTGGGATTCACAACGATAAATGTCAATGAATACTAATAGACTAATTAAGGCAATTTGAT 840
DB 541 TGGGGATTCACAACGATAAATGTCAATGAATACTAATAGACTAATTAAGGCAATTTGAT 600
QY 841 GAATATGCTGATCAGTGCATACGTATATACGGGGATTAATTAATTTTACCGAATCT 900
DB 601 GAATATGCTGATCAGTGCATACGTATATACGGGGATTAATTAATTTTACCGAATCT 660
QY 901 AGCTATCAAGATTTGGATAACATATATCGATACGGAGAGACTTAACATTTGACTGTATTA 960
DB 661 AGCTATCAAGATTTGGATAACATATATCGATACGGAGAGACTTAACATTTGACTGTATTA 720
QY 961 GATATCGCGCTTTCTTTCCAAACTATGACAAATAGAGATATCCAAATTCAGCGAGTTGGT 1020
DB 721 GATATCGCGCTTTCTTTCCAAACTATGACAAATAGAGATATCCAAATTCAGCGAGTTGGT 780
QY 1021 CAACTAACAGGAGAGTTATACGGACCAATTAATTTAATTTTAAATCCAGTTACAGTCT 1080
DB 781 CAACTAACAGGAGAGTTATACGGACCAATTAATTTAATTTTAAATCCAGTTACAGTCT 840
QY 1081 GTAGCTCAATTAACCTTTTAACTGTTAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB 841 GTAGCTCAATTAACCTTTTAACTGTTAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 1141 TTTGATATATGAATTAATCTTACAAATCTTTTACGGATTTGGTTAGTTGGAGCGCAATTTT 1200
DB 901 TTTGATATATGAATTAATCTTACAAATCTTTTACGGATTTGGTTAGTTGGAGCGCAATTTT 960
QY 1201 TATTTGGGAGGACATCGAGTATATCTAGCTTATAGGAGTGGTAAATACATCATCTCTCT 1260
DB 961 TATTTGGGAGGACATCGAGTATATCTAGCTTATAGGAGTGGTAAATACATCATCTCTCT 1020
QY 1261 ATATATGGAAGAGAGCGCAACAGGAGCTTCAAGATCTTTTAAATGCAAGCGGTA 1320
DB 1021 ATATATGGAAGAGAGCGCAACAGGAGCTTCAAGATCTTTTAAATGCAAGCGGTA 1080
QY 1321 TTTAGGACTTTATCAATCTCTTCTTAACTGAAATTAATGAGCACTTTGCGAGCGCACCAT 1380
DB 1081 TTTAGGACTTTATCAATCTCTTCTTAACTGAAATTAATGAGCACTTTGCGAGCGCACCAT 1140
QY 1381 TTTAATTTACGTTGGTGAAGAGTAGAATTTTCTACCTTACAAATAGCTTTTAGTAT 1440
DB 1141 TTTAATTTACGTTGGTGAAGAGTAGAATTTTCTACCTTACAAATAGCTTTTAGTAT 1200
QY 1441 GCAGGAAGAGGTACGTTGATTTCTTTAACTGAAATTAATGAGCACTTTGCGAGCGCACCAT 1500
DB 1201 GCAGGAAGAGGTACGTTGATTTCTTTAACTGAAATTAATGAGCACTTTGCGAGCGCACCAT 1260
QY 1501 CCTCGGAAGGATATAGTCATCGTTTATGTGTCACAACTTTTGTTCAAAGATCTGGAACA 1560

DB 1261 CCTCGGAAGGATATAGTCATCGTTTATGTGTCACAACTTTTGTTCAAAGATCTGGAACA 1320
QY 1561 CTTTTTTTTTAAACAATCGTTGTAGTATTTCTTCGACGCACTCGTAGTGCACATCTTTACAAAT 1620
DB 1321 CTTTTTTTTTAAACAATCGTTGTAGTATTTCTTCGACGCACTCGTAGTGCACATCTTTACAAAT 1380
QY 1621 ACAATTTGATCCAGAGAGAAATTAATCAAAATCACTTTTAGTGAAAGGATTTAGAGTTTGGGG 1680
DB 1381 ACAATTTGATCCAGAGAGAAATTAATCAAAATCACTTTTAGTGAAAGGATTTAGAGTTTGGGG 1440
QY 1681 GGCACCTCTGTCTATTACAGGACCAAGATTTACAGAGGGGATATCCTTCGAGAGAAATACC 1740
DB 1441 GGCACCTCTGTCTATTACAGGACCAAGATTTACAGAGGGGATATCCTTCGAGAGAAATACC 1500
QY 1741 TTTGTGTATTTGTATCTCTCAAACTCAATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1800
DB 1501 TTTGTGTATTTGTATCTCTCAAACTCAATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1560
QY 1801 TTAAGATTTCTGTACGCTTCCAGTAGGATGAGAGTTATAGTATTAATTAATTAATTAATTAATTAAT 1860
DB 1561 TTAAGATTTCTGTACGCTTCCAGTAGGATGAGAGTTATAGTATTAATTAATTAATTAATTAATTAAT 1620
QY 1861 TCCACAGAGTGGGAGGCAAGTTAGTGTAGATATGCTCTTTCAGAGAACTATGGAATA 1920
DB 1621 TCCACAGAGTGGGAGGCAAGTTAGTGTAAATATATGCTCTTTCAGAGAACTATGGAATA 1680
QY 1921 GGGGAGAACTTTAACTATAGAACATTTAGATATACGATTTTGTAGTAATCTTTTTCATTT 1980
DB 1681 GGGGAGAACTTTAACTATAGAACATTTAGATATACGATTTTGTAGTAATCTTTTTCATTT 1740
QY 1981 AGAGCTAATCCAGATATTAATTTGGGATAAGTGAACAACTCTATTTGGTGCAGGTTCTATT 2040
DB 1741 AGAGCTAATCCAGATATTAATTTGGGATAAGTGAACAACTCTATTTGGTGCAGGTTCTATT 1800
QY 2041 AGTAGCGTTGAACCTTTTATATAGATAAAATTTGAAATTTTCTAGAGATGCAACATTTGAA 2100
DB 1801 AGTAGCGTGAACCTTTTATATAGATAAAATTTGAAATTTTCTAGAGATGCAACATTTGAA 1860
QY 2101 CGAGAACTCTGATTTTGAAGAGACAAAGGCGGTGAATGCTTCTTCTTCCAT 2160
DB 1861 CGAGAACTCTGATTTTGAAGAGAGACAAAGGCGGTGAATGCTTCTTCTTCCAT 1920
QY 2161 CAAATCGGTTTAAACCCGATGACGATATCATATTTGATCAAGTATCCAATTTAGTG 2220
DB 1921 CAAATCGGTTTAAACCCGATGACGATATCATATTTGATCAAGTATCCAATTTAGTG 1980
QY 2221 GATTTTATCAGATGAATTTTGTCTGATGAAAGCGAGAAATTTCTCGAGAGAAAGTCAAA 2280
DB 1981 GATTTTATCAGATGAATTTTGTCTGATGAAAGCGAGAAATTTCTCGAGAGAAAGTCAAA 2040
QY 2281 CATCGAAGCGACTCAGTGTAGCGGAAATTTTACTTTCAAGATCCAACTTCAGAGGGATC 2340
DB 2041 CATCGAAGCGACTCAGTGTAGCGGAAATTTTACTTTCAAGATCCAACTTCAGAGGGATC 2100
QY 2341 AATAGAACACAGACCGTGGCTGGAGAGAGATGACAGATATTAATTAATTAATTAATTAATTAATTAAT 2400
DB 2101 AATAGAACACAGACCGTGGCTGGAGAGAGATGACAGATATTAATTAATTAATTAATTAATTAATTAAT 2160
QY 2401 GACGTATTTCAAAGAGAAATTTACGTCACTACCTCGGGTACCGTTGATGAGTGTATCCAAG 2460
DB 2161 GACGTATTTCAAAGAGAAATTTACGTCACTACCTCGGGTACCGTTGATGAGTGTATCCAAG 2220
QY 2461 TATTTATATCAGAAATAGATGAGTGCAGAAATTTAAAGCTTATACCCGTTATGAATTAAGA 2520
DB 2221 TATTTATATCAGAAATAGATGAGTGCAGAAATTTAAAGCTTATACCCGTTATGAATTAAGA 2280
QY 2521 GGGTATATCGAAGTAGTCAAGACTTTAGAAATCTATTTTGTATGCTGCGGTGCAATGCAAAACAC 2580
DB 2281 GGGTATATCGAAGTAGTCAAGACTTTAGAAATCTATTTTGTATGCTGCGGTGCAATGCAAAACAC 2340
QY 2581 GAAATAGTAAATGTGCCAGGACCGGTTCTTTATGCGCGCTTTTACGCCCAAGTCCAATC 2640

Db	2341	GAATAGTAATGTGCCAGGACGGGTTCTTATGCGCGCTTCAGGCCAAGTCCAAATC	2400
Qy	2641	GGAAAGTGTGGAGAACCGAATCGATCGCGGCCACACCTTGATGGAAATCTGATCTAGAT	2700
Db	2401	GGAAAGTGTGGAGAACCGAATCGATCGCGGCCACACCTTGATGGAAATCTGATCTAGAT	2460
Qy	2701	TGTTCTCTGCAG 2711	
Db	2461	TGTTCTCTGCAG 2471	
RESULT 10			
AAX80019			
ID	AAX80019 standard; DNA; 3567 BP.		
AC	AAX80019;		
XX	12-AUG-1999 (first entry)		
DT	B. thuringiensis crystal protein CryIC-R148A nucleotide sequence.		
XX	Bacillus thuringiensis; delta-endotoxin; insecticide; crystal protein;		
KW	lepidopteran insect; CryIC; genetic engineering; mutagenesis; mutant;		
KW	caterpillar; beetle; mosquito; toxic; modification; ss.		
XX	Bacillus thuringiensis.		
OS	Synthetic.		
XX	US5914318-A.		
PN	22-JUN-1999.		
PD	26-NOV-1997; 97US-0980071.		
PF	26-NOV-1997; 97US-0980071.		
PR	27-NOV-1996; 96US-0757536.		
XX	(ECOG-) ECOGEN INC.		
PA	Baum JA, Gilmer AJ, Mettuss AL;		
XX	WPI; 1999-370510/31.		
PI	P-PSDB; AAY17788.		
DR	New modified delta-endotoxin crystal proteins from Bacillus		
PT	thuringiensis are useful in insecticidal compositions		
XX	Example 5; Column 97-99; 144pp; English.		
PS	The present invention describes a new composition comprising an isolated		
XX	polypeptide for modified Bacillus thuringiensis crystal proteins (CryIC).		
CC	The polypeptide of the composition is insecticidally-active against		
CC	Lepidoptera. The composition is toxic to an insect cell and comprised		
CC	within an insecticidal formulation can be used as a plant protective		
CC	spray which is toxic to caterpillars, beetles and mosquitoes. The		
CC	polypeptide of the composition may be used to kill an insect through		
CC	ingestion of the composition directly or by ingestion of a plant coated		
CC	with the composition or a transgenic plant that expresses the polypeptide		
CC	composition. The insecticidal proteins produced by B. thuringiensis are		
CC	harmless to plants and other non-targeted organisms but toxic to their		
CC	specific target insect. The polypeptides have improved toxicity so a		
CC	reduced amount of bioinsecticide per unit area of treated crop can be		
CC	used allowing economic and efficient utilization in the field. The		
CC	present sequence encodes a modified B. thuringiensis crystal protein.		
XX	Sequence 3567 BP; 1168 A; 597 C; 791 G; 1011 T; 0 other;		
SQ			
Query Match 89.6%; Score 2429.4; DB 20; Length 3567;			
Best Local Similarity 98.9%; Pred. No. 0;			
Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;			
Qy	241	ATGAGAGAAATATCAAAATCAATGCATCTACCTTACATTTGTTAAGTAAATCCTGAAGAA	300

Seq	Sequence	3567 BP; 1168 A; 597 C; 791 G; 1011 T; 0 other;	Qy
Qy	Query Match	89.6%; Score 2429.4; DB 21; Length 3567;	
Db	Best Local Similarity	98.9%; Pred. No. 0;	
Db	Matches 2445; Conservative	0; Mismatches 26; Indels 0; Gaps 0;	
Qy	241	ATGAGAGAAATAATCAAAATCAATGATACCTTACAAATTTTAAAGTATCCTGAAGAA 300	
Db	1	ATGAGAGAAATAATCAAAATCAATGATACCTTACAAATTTTAAAGTATCCTGAAGAA 60	
Qy	301	GTACTTTTGGATGGAGACCGATCAACTGGTAAATTAATCAATTCATATTTCTGTCTCA 360	
Db	61	GTACTTTTGGATGGAGACCGATCAACTGGTAAATTCATCAATTCATATTTCTGTCTCA 120	
Qy	361	CTTGTTGAGTTCTGCTATCTAACTTTGTACACAGGGGAGGATTTTGTGATTAATA 420	
Db	121	CTTGTTGAGTTCTGCTATCTAACTTTGTACACAGGGGAGGATTTTGTGATTAATA 180	
Qy	421	GATTTTGTATGGGATAGTTGGCCCTTCTCAATGGGATGATTTCTAGTACAAATGAA 480	
Db	181	GATTTTGTATGGGATAGTTGGCCCTTCTCAATGGGATGATTTCTAGTACAAATGAA 240	
Qy	481	CAATTAATTAATGAAGAATAGCTGAATTTCTGAGAAATGCTGCTATTCGTAATTTAGAA 540	
Db	241	CAATTAATTAATGAAGAATAGCTGAATTTCTGAGAAATGCTGCTATTCGTAATTTAGAA 300	
Qy	541	GGATTAGGAAACAAATTTCAATATATATGTTGGAAGCATTTAAAGATGGGAGAGATCCT 600	
Db	301	GGATTAGGAAACAAATTTCAATATATATGTTGGAAGCATTTAAAGATGGGAGAGATCCT 360	
Qy	601	AATAATCCAGCAACAGGACACAGAGTAATGATCGCTTTGCTATCTGATGAGGCTACTT 660	
Db	361	AATAATCCAGCAACAGGACACAGAGTAATGATCGCTTTGCTATCTGATGAGGCTACTT 420	
Qy	661	GAAAGGGAACATTTCTCGTTTGGAAATTTCTGGAATTTGAAAGTACCCCTTTATCCGTTTAT 720	
Db	421	GAAAGGGAACATTTCTCGTTTGGAAATTTCTGGAATTTGAAAGTACCCCTTTATCCGTTTAT 480	
Qy	721	GCTCAAGCGGCCCAATCTGCAATCTAGCTATATAAGAGATTTCTGTAATTTTGGAGAAAGA 780	
Db	481	GCTCAAGCGGCCCAATCTGCAATCTAGCTATATAAGAGATTTCTGTAATTTTGGAGAAAGA 540	
Qy	781	TTGGGATTCGACAGGATAAATGTCAATGAAACTATAAATAGACTAAATTTAGGCATATTGAT 840	
Db	541	TGGGGATTCGACAGGATAAATGTCAATGAAACTATAAATAGACTAAATTTAGGCATATTGAT 600	
Qy	841	GAATATGCTGATCACTGTGCAATAGATTAATCGGGATTAATAATTTACCGAAATCT 900	
Db	601	GAATATGCTGATCACTGTGCAATAGATTAATCGGGATTAATAATTTACCGAAATCT 660	
Qy	901	ACGATATCAAGATTGATTAACATATATCGATTAATCGGAGACCTTAACATGACTGTATTA 960	
Db	661	ACGATATCAAGATTGATTAACATATATCGATTAATCGGAGACCTTAACATGACTGTATTA 720	
Qy	961	GATATCCCGCTTTCTTTCCAACTATGACAAATAGAGATATCCAAATTCAGCCAGTTGGT 1020	
Db	721	GATATCCCGCTTTCTTTCCAACTATGACAAATAGAGATATCCAAATTCAGCCAGTTGGT 780	
Qy	1021	CNACTAAACAGGGAAGTTTATACCGACCAATTAATTAATTTTAACTCCAGTTACAGTCT 1080	
Db	781	CNACTAAACAGGGAAGTTTATACCGACCAATTAATTAATTTTAACTCCAGTTACAGTCT 840	
Qy	1081	GTAGTCTCAATTTACTTCTTTAAAGTTTATGGAGACGCGCAATTTAGAAATCTCTATTA 1140	
Db	841	GTAGTCTCAATTTACTTCTTTAAAGTTTATGGAGACGCGCAATTTAGAAATCTCTATTA 900	
Qy	1141	TTTGATATTTGAAATTAATCTTACCAATCTTTAGCGAATTTGGTTAGTGTGGACGCAATTTT 1200	
Db	901	TTTGATATTTGAAATTAATCTTACCAATCTTTAGCGAATTTGGTTAGTGTGGACGCAATTTT 960	
Qy	1201	TATTCGGGAGGACATCGATTAATCTAGCGCTTTATAGGAGGTGGTAAACATATCTCCT 1260	
Db	961	TATTCGGGAGGACATCGATTAATCTAGCGCTTTATAGGAGGTGGTAAACATATCTCCT 1020	

QY 2341 AATAGACAACACCGCTGCTGGAGAGGAGTACAGATATTAACCATCCAGGAGGAT 2400
 Db AATAGACAACACCGCTGCTGGAGAGGAGTACAGATATTAACCATCCAGGAGGAT 2160
 QY 2401 GACGTATTTCAAGAGAAATACGTCACACTACCGGCTACCGTTGATGAGTCTATCCACG 2460
 Db GACGTATTTCAAGAGAAATACGTCACACTACCGGCTACCGTTGATGAGTCTATCCACG 2220
 QY 2461 TATTTATATCAGAAATATAGATGAGTCAAAATTAAGCTTATATACCGTTATGAATTAAGA 2520
 Db TATTTATATCAGAAATATAGATGAGTCAAAATTAAGCTTATATACCGTTATGAATTAAGA 2280
 QY 2521 GGTATATCAGAGATAGTCAAGCTTAGAATCTATTGATCGGTACATGCAATCAACAC 2580
 Db GGTATATCAGAGATAGTCAAGCTTAGAATCTATTGATCGGTACATGCAATCAACAC 2340
 QY 2581 GAAATAGTAAATGTCCAGGACCGGTTCTTATGCGCGCTTTTCAGCCCAAGCTCCAATC 2640
 Db GAAATAGTAAATGTCCAGGACCGGTTCTTATGCGCGCTTTTCAGCCCAAGCTCCAATC 2400
 QY 2641 GGAAGTGTGGAGAACCGAATCGATCGCGCCACACCTTTGAATGGAATCCTGATCTAGAT 2700
 Db GGAAGTGTGGAGAACCGAATCGATCGCGCCACACCTTTGAATGGAATCCTGATCTAGAT 2460
 QY 2701 TGTTCCTGCAG 2711
 Db TGTTCCTGCAG 2471

RESULT 12

AA08149
 ID AAA08149 standard; DNA; 3567 BP.
 AC AAA08149;
 XX
 DT 27-JUN-2000 (first entry)
 XX
 DE Bacillus thuringiensis CryIC.499 gene SEQ ID NO:11.
 XX
 KW Bacillus thuringiensis; CryIC; crystal protein; insecticide; insect;
 KW delta-endotoxin; lepidopteran; modification; genetic engineering;
 KW resistance; mutant; mutagenesis; ss.
 XX
 OS Bacillus thuringiensis.
 OS Synthetic.
 XX
 PN US6033874-A.
 XX
 PD 07-MAR-2000.
 XX
 PF 18-MAY-1999; 99US-0314093.
 XX
 PR 26-NOV-1997; 97US-0980071.
 PR 27-NOV-1996; 96US-0757536.
 XX
 PA (ECOG-) ECOGEN INC.
 XX
 PI Mettuss AL, Baum JA, Gilmer AJ;
 XX
 DR WPI; 2000-255697/22.
 DR P-PSDB; AAY82401.
 XX
 PT New mutant Bacillus thuringiensis endotoxin, used for controlling
 PT lepidopteran pests, has mutated loop region to impart higher
 PT insecticidal activity -
 XX
 PS Example 14; Column 119-122; 153pp; English.
 XX
 CC The present invention describes isolated Bacillus thuringiensis CryIC
 CC delta-endotoxin polypeptides having: (i) at least one amino acid (aa)
 CC mutation in the loop region between alpha-helices 6 and 7 of domain 1;
 CC and (ii) better activity against lepidoptera than the native CryIC.
 CC The polypeptides, possibly after activation in the digestive tract of

CC insects, kills insect cells by formation of pores and disturbing
 CC cellular homeostasis. The polypeptides are used to control lepidopteran
 CC pests on plants, either: (i) applied as a composition; or (ii) expressed
 CC in plants from heterologous nucleic acid (generating insect-resistant
 CC plants). They are more active against lepidoptera than native CryIC.
 CC AAA08144 to AAA08182, and AAY82396 to AAY82432, represent sequences used
 CC in the exemplification of the present invention.

XX SQ Sequence 3567 BP; 1167 A; 599 C; 791 G; 1010 T; 0 other;

Query Match 89.6%; Score 2429.4; DB 21; Length 3567;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
 QY 241 ATGGAGGAAAATAAATCAAAATCAATGCATACCTTACAAATGTTTAAAGTAAATCCTGAAGAA 300
 Db 1 ATGGAGGAAAATAAATCAAAATCAATGCATACCTTACAAATGTTTAAAGTAAATCCTGAAGAA 60
 QY 301 GTACTTTTGGATGGAGAACGGATATCAACTGGTAATCTCAATTTGATATTTCTGTCTCA 360
 Db 61 GTACTTTTGGATGGAGAACGGATATCAACTGGTAATCTCAATTTGATATTTCTGTCTCA 120
 QY 361 CTTGTTTCAGTTTCTGGTATCTAACTTTGTACACGGGGGAGGATTTTGTAGTGAATTAATA 420
 Db 121 CTTGTTTCAGTTTCTGGTATCTAACTTTGTACACGGGGGAGGATTTTGTAGTGAATTAATA 180
 QY 421 GATTTTGTATGGGGAATAGTTCGCCCTTCTCAATGGGATGCATTTCTAGTACAAATTTGAA 480
 Db 181 GATTTTGTATGGGGAATAGTTCGCCCTTCTCAATGGGATGCATTTCTAGTACAAATTTGAA 240
 QY 481 CAATTAATTAATGAAGAATAGTCTGAATTTGCTAGGAATGCTGCTATTTCTAATTTAGAA 540
 Db 241 CAATTAATTAATGAAGAATAGTCTGAATTTGCTAGGAATGCTGCTATTTCTAATTTAGAA 300
 QY 541 GGAATAGGAACAATTTCAATATATATGTGGAGCAATTTAAAGAATGGGAAGAGATCCT 600
 Db 301 GGAATAGGAACAATTTCAATATATATGTGGAGCAATTTAAAGAATGGGAAGAGATCCT 360
 QY 601 AATAATCCAGCAACACGAGACAGAGTAATTTGATCGCTTTTCGTATATCTTCAATGGCTACT 660
 Db 361 CATATCCAGCAACACGAGACAGAGTAATTTGATCGCTTTTCGTATATCTTCAATGGCTACT 420
 QY 661 GAAAGGACATTCCTTCGTTTCGAATTTCTGGAATTTGAAGTACCCCTTTTATCCGTTTAT 720
 Db 421 GAAAGGACATTCCTTCGTTTCGAATTTCTGGAATTTGAAGTACCCCTTTTATCCGTTTAT 480
 QY 721 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTCGTAAATTTTGGAGAAAGA 780
 Db 481 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTCGTAAATTTTGGAGAAAGA 540
 QY 781 TTGGGATTTGACAACGATAAATGCTCAATGAAAATTAATAGACTAATTAGGCATATTTGAT 840
 Db 541 TTGGGATTTGACAACGATAAATGCTCAATGAAAATTAATAGACTAATTAGGCATATTTGAT 600
 QY 841 GAATATGCTGATCACTGTGCAAAATACGTATATTCGGGATTAATAATTTACCGAAATCT 900
 Db 601 GAATATGCTGATCACTGTGCAAAATACGTATATTCGGGATTAATAATTTACCGAAATCT 660
 QY 901 ACGTATCAAGATTTGGATTAACATATATCGATTACGAGAGACTTAACATTTGATTTA 960
 Db 661 ACGTATCAAGATTTGGATTAACATATATCGATTACGAGAGACTTAACATTTGATTTA 720
 QY 961 GATATCGCGGCTTTCTTTCCAACTATGCAATAGAGATATCCAAATTCAGCAGTTGGT 1020
 Db 721 GATATCGCGGCTTTCTTTCCAACTATGCAATAGAGATATCCAAATTCAGCAGTTGGT 780
 QY 1021 CAACCTAACAGGGAAGTTTATACGGACCCATTAATTAATTTTAAATCCACAGTTACAGTCT 1080
 Db 781 CAACCTAACAGGGAAGTTTATACGGACCCATTAATTAATTTTAAATCCACAGTTACAGTCT 840
 QY 1081 GTAGTCTCAATTTACCTACTCTTTTAACTTATGGAGAGACGCGCAATTTAGAAATCCTCATTTA 1140
 Db 841 GTAGTCTCAATTTACCTACTCTTTTAACTTATGGAGAGACGCGCAATTTAGAAATCCTCATTTA 900

Qy	1141	TTTGATATATCGAATTAATCTTACAACTTTTACGGATTGGTTAGTTGGAGCAATTTT	1200
Db	901	TTTGATATATCGAATTAATCTTACAACTTTTACGGATTGGTTAGTTGGAGCAATTTT	960
Qy	1201	TATTGGGAGGACATCGAGTAATATCTAGCTTTATAGGAGTGGTAAACATAACATCTCCT	1260
Db	961	TATTGGGAGGACATCGAGTAATATCTAGCTTTATAGGAGTGGTAAACATAACATCTCCT	1020
Qy	1261	ATATATGAGAGAGGCGCAACACGAGGCTCCAAAGATCTTTTAAATGGACCGGTA	1320
Db	1021	ATATATGAGAGAGGCGCAACACGAGGCTCCAAAGATCTTTTAAATGGACCGGTA	1080
Qy	1321	TTTAGGACTTTATCAATTCCTACTTTACGATTATACAGCAACTTCCGAGCGCCACAT	1380
Db	1081	TTTAGGACTTTATCAATTCCTACTTTACGATTATACAGCAACTTCCGAGCGCCACCA	1140
Qy	1381	TTTAAATTTAGCTGGTGGAGGAGTAGAATTTCTACACCTCAAAATAGCTTTACGTAT	1440
Db	1141	TTTAAATTTAGCTGGTGGAGGAGTAGAATTTCTACACCTCAAAATAGCTTTACGTAT	1200
Qy	1441	GCAGAGAGAGGTAACGTTGATCTTTAACTGAATTTACCGCTGAGGATAATAGTGTGCA	1500
Db	1201	CGAGAGAGAGGTAACGTTGATCTTTAACTGAATTTACCGCTGAGGATAATAGTGTGCA	1260
Qy	1501	CCTCGGAGAGATATAGTCACTGTTTATGTCATGCACTTTTGTTCAGAGATCTGACACA	1560
Db	1261	CCTCGGAGAGATATAGTCACTGTTTATGTCATGCACTTTTGTTCAGAGATCTGACACA	1320
Qy	1561	CCTTTTAAACAACTGGTGTAGTATTTCTTGTGACGATTCGTAGTGCMACTCTTCAAAAT	1620
Db	1321	CCTTTTAAACAACTGGTGTAGTATTTCTTGTGACGATTCGTAGTGCMACTCTTCAAAAT	1380
Qy	1621	ACAAATGATCCAGAGAGAAATTAATCAATACCTTTAGTGAAGAGATTTAGTTGGGGG	1680
Db	1381	ACAAATGATCCAGAGAGAAATTAATCAATACCTTTAGTGAAGAGATTTAGTTGGGGG	1440
Qy	1681	GGCACCCTGTCATTACAGGACGAGATTTACAGGAGGGATTCCTTCGAAGAAATACC	1740
Db	1441	GGCACCCTGTCATTACAGGACGAGATTTACAGGAGGGATTCCTTCGAAGAAATACC	1500
Qy	1741	TTTGGTGAATTTGTATCTCTACAACTCAATTAATTAATTCACCAATTTACCAAGATACCGT	1800
Db	1501	TTTGGTGAATTTGTATCTCTACAACTCAATTAATTAATTCACCAATTTACCAAGATACCGT	1560
Qy	1801	TTAAGATTTCTGTACGCTTCCAGTAGGATGCAGAGTTATAGTATTAACAGAGCGGCA	1860
Db	1561	TTAAGATTTCTGTACGCTTCCAGTAGGATGCAGAGTTATAGTATTAACAGAGCGGCA	1620
Qy	1861	TCCACAGGAGTGGGAGCGCAAGTTAGTGTAGATATGCTCTTCAGAAATCTATGGAATA	1920
Db	1621	TCCACAGGAGTGGGAGCGCAAGTTAGTGTAGATATGCTCTTCAGAAATCTATGGAATA	1680
Qy	1921	GGGGAGACTTAACATCTAGAACATTTAGATATACCGATTTAGTAATCTTTTTCATTT	1980
Db	1681	GGGGAGACTTAACATCTAGAACATTTAGATATACCGATTTAGTAATCTTTTTCATTT	1740
Qy	1981	AGAGCTAATCCAGATATATTTGGGATAGTGAACCTCTATTTGGTGCAGGTTCTATT	2040
Db	1741	AGAGCTAATCCAGATATATTTGGGATAGTGAACCTCTATTTGGTGCAGGTTCTATT	1800
Qy	2041	AGTAGCGTTGAATTTATATAGATAAATTTGAATTTATCTAGCAGATCAACATTTGAA	2100
Db	1801	AGTAGCGTTGAATTTATATAGATAAATTTGAATTTATCTAGCAGATCAACATTTGAA	1860
Qy	2101	GCAGAACTGTATTTAGAAAGAGCAAAAAGCGGTGAATGCTCTTCTTCTTCCAAAT	2160
Db	1861	GCAGAACTGTATTTAGAAAGAGCAAAAAGCGGTGAATGCTCTTCTTCTTCCAAAT	1920
Qy	2161	CAAAATCGGGTTAAAAACCGATGTGACGGATTATCATTTATGATCAAGTCCAAATTTAGT	2220
Db	1921	CAAAATCGGGTTAAAAACCGATGTGACGGATTATCATTTATGATCAAGTCCAAATTTAGT	1980
Qy	2221	GATCTTTATCAGATCAATTTTGTCTGGATGAAAGCGAGAAATTTGTCGAGAAAGTCAAA	2280
Db	1981	GATCTTTATCAGATCAATTTTGTCTGGATGAAAGCGAGAAATTTGTCGAGAAAGTCAAA	2040
Qy	2281	CATCGAGGAGCTCAGTGTATGAGCGGAATTTACTTTCAAGATCCAAATTTCAAGGGATC	2340
Db	2041	CATCGAGGAGCTCAGTGTATGAGCGGAATTTACTTTCAAGATCCAAATTTCAAGGGATC	2100
Qy	2341	ATATAGCAACACGAGACCTGGCTGGAGAGGAGTACAGATATTTACCATCCAGGAGGAGAT	2400
Db	2101	ATATAGCAACACGAGACCTGGCTGGAGAGGAGTACAGATATTTACCATCCAGGAGGAGAT	2160
Qy	2401	GAGCTATTTCAAGAGAAATTTACGTCACACTACCGGTACCGTTGATGAGTGTATCCAAAG	2460
Db	2161	GAGCTATTTCAAGAGAAATTTACGTCACACTACCGGTACCGTTGATGAGTGTATCCAAAG	2220
Qy	2461	TATTTATATCAAGAAATTTAGTGTAGTGTGAATTAAGCTTTATACCGTTTATGAATTAAGA	2520
Db	2221	TATTTATATCAAGAAATTTAGTGTAGTGTGAATTAAGCTTTATACCGTTTATGAATTAAGA	2280
Qy	2521	GGTATATCGAAGATAGTCAAGACTTAGAATCTTATTTGATCGTTACAAATGCAAAACAC	2580
Db	2281	GGTATATCGAAGATAGTCAAGACTTAGAATCTTATTTGATCGTTACAAATGCAAAACAC	2340
Qy	2581	GAAATAGTAAATTTGCCAGACGGTTCCTTATGCGCGCTTCAGCCCAAGTCCCAATC	2640
Db	2341	GAAATAGTAAATTTGCCAGACGGTTCCTTATGCGCGCTTCAGCCCAAGTCCCAATC	2400
Qy	2641	GGAAGTGTGGAGAACCGAATCGATGCGCGCACACCTTGATGGAATCTCTGATCTAGAT	2700
Db	2401	GGAAGTGTGGAGAACCGAATCGATGCGCGCACACCTTGATGGAATCTCTGATCTAGAT	2460
Qy	2701	TGTTCTCTCGAG 2711	
Db	2461	TGTTCTCTCGAG 2471	

RESULT 13

AAD44210

AD44210 standard; DNA; 3567 BP.

AC

AD44210;

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Bacillus thuringiensis Cry1C-R148A mutant protein encoding DNA.
Cry1 protein; delta-endotoxin; insect resistance; lepidopteran insect;
transgenic plant; transgenic; mutant; gene; ds.

Key Location/Qualifiers

CDS 1..3567

/*tag= a

/product= "CRY1C-R148A mutant protein"

/notes= "No stop codon"

/partial

US6313378-B1.

06-NOV-2001.

21-JUN-1999; 99US-0337635.

26-NOV-1997; 97US-0980071.

27-NOV-1996; 96US-0757536.

(MONS) MONSANTO TECHNOLOGY LLC.

Baum JA, Gilmer AJ, Mettus AL;

DR WPI; 2002-033341/04.
XX P-PSDB; ARE26460.
PT Transgenic plants, comprises nucleic acid encoding CryIc
PT delta-endotoxin polypeptide, has improved resistance to Lepidopteran
PT insects
XX
XX Example 5; Column 131-140; 15lpp; English.
XX The present invention relates to novel transgenic plants comprising CryI
CC delta-endotoxin genes, in particular cryIc genes that encode modified
CC crystal proteins having improved resistance to Lepidopteran insects. The
CC plants that express the mutated CryIc delta-endotoxin crystal proteins
CC are monocotyledonous (corn, wheat, oat, rice, barley, turf grass, pasture
CC grass) or dicotyledonous (legume, soybean, cotton, fruit, berry, tree).
CC The present sequence is a DNA encoding *Bacillus thuringiensis* CryIc-R148A
CC mutant protein.
XX
XX Sequence 3567 BP; 1168 A; 597 C; 791 G; 1011 T; 0 other;
SQ
Query Match 89.6%; Score 2429.4; DB 24; Length 3567;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 241 ATGAGGAAATTAATCAAAATCAATGCATACCTTACAAATGTTTAAAGTAATCTCGAAGAA 300
DB 1 ATGAGGAAATTAATCAAAATCAATGCATACCTTACAAATGTTTAAAGTAATCTCGAAGAA 60
QY 301 GTACTTTTGGATGGAGACCGGATATCAACTGGTAATTAATCAATGCATATTTCTCTGTCA 360
DB 61 GTACTTTTGGATGGAGACCGGATATCAACTGGTAATTAATCAATGCATATTTCTCTGTCA 120
QY 361 CTGTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTT 420
DB 121 CTGTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTT 180
QY 421 GATTTTGTATGGGAATAGTGGCCCTTCTCAATGGATGCAATTTCTAGTACAAATGAA 480
DB 181 GATTTTGTATGGGAATAGTGGCCCTTCTCAATGGATGCAATTTCTAGTACAAATGAA 240
QY 481 CAATTAATTAATGAAGAATAGTGGATTTGCTAGGAATGCTGCTAATTTCTAATTTAGAA 540
DB 241 CAATTAATTAATGAAGAATAGTGGATTTGCTAGGAATGCTGCTAATTTCTAATTTAGAA 300
QY 541 GGATTAGGAAACAAATTTCAATATATATGTGGAAGCAATTTAAAGAAATGGGAAGATCCT 600
DB 301 GGATTAGGAAACAAATTTCAATATATATGTGGAAGCAATTTAAAGAAATGGGAAGATCCT 360
QY 601 AATAATCCAGCAACAGGACCGAGTAATGTATGATGCTTTTCTGATATCTGATGGCTACTT 660
DB 361 AATAATCCAGCAACAGGACCGAGTAATGTATGATGCTTTTCTGATATCTGATGGCTACTT 420
QY 661 GAAAGGCAATTCCTTCGTTTCGAATTTCTGGAATTTGGAAGTACCCCTTTTATCCGTTTAT 720
DB 421 GAAAGGCAATTCCTTCGTTTCGAATTTCTGGAATTTGGAAGTACCCCTTTTATCCGTTTAT 480
QY 721 GCTCAAGCGCCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTGGAGAAAGA 780
DB 481 GCTCAAGCGCCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTGGAGAAAGA 540
QY 781 TTGGGATTCGAAACGATAAATGTCAATGAATACTATAATAGACTAATATTAGGCATATTGAT 840
DB 541 TTGGGATTCGAAACGATAAATGTCAATGAATACTATAATAGACTAATATTAGGCATATTGAT 600
QY 841 GAATATGCTGATCCTTCGTTTCGAATTTCTGGAATTTGGAAGTACCCCTTTTATCCGTTTAT 900
DB 601 GAATATGCTGATCCTTCGTTTCGAATTTCTGGAATTTGGAAGTACCCCTTTTATCCGTTTAT 660
QY 901 AGCTATCAAGATTTGGATAACATATATCGATTACGGAGAGACTTAAACATTGTGATTTA 960
DB 661 AGCTATCAAGATTTGGATAACATATATCGATTACGGAGAGACTTAAACATTGTGATTTA 720
QY 961 GATATGCGCGCTTTCTTTCCAAACTATATGACAAATAGGAGATATCCAAATTCAGCCAGTTGTT 1020

DB 721 GATATGCGCGCTTTCTTTCCAAACTATGACAAATAGGAGATATCCAAATTCAGCCAGTTGTT 780
QY 1021 CCACTAAACAGGGAAGTTTATACGGACCCCAATTAATTAATTTAATCCACAGTTTACAGTCT 1080
DB 781 CCACTAAACAGGGAAGTTTATACGGACCCCAATTAATTAATTTAATCCACAGTTTACAGTCT 840
QY 1081 GTAGCTCAATTAACCTACTTTTAACTGATGAGAGCAGCGCAATTAAGAAATCTCATTTA 1140
DB 841 GTAGCTCAATTAACCTACTTTTAACTGATGAGAGCAGCGCAATTAAGAAATCTCATTTA 900
QY 1141 TTTGATATATTAATTAATCTTACAAATCTTTACGGATGTTTGTAGTGTGGAGCGCAATTTT 1200
DB 901 TTTGATATATTAATTAATCTTACAAATCTTTACGGATGTTTGTAGTGTGGAGCGCAATTTT 960
QY 1201 TATTTGGGAGGACATCGAGTATATCTAGCCTTTATAGGAGGTGGTAACATACATCTCCT 1260
DB 961 TATTTGGGAGGACATCGAGTATATCTAGCCTTTATAGGAGGTGGTAACATACATCTCCT 1020
QY 1261 ATATATGGAAGAGAGCGGAAACAGGAGCCTCCAAGATCTCTTTACTTTTAAATGACCGGTA 1320
DB 1021 ATATATGGAAGAGAGCGGAAACAGGAGCCTCCAAGATCTCTTTACTTTTAAATGACCGGTA 1080
QY 1321 TTTAGGACTTTTATCAATCTTCTACTTTTACGATTTATTAACAGAACTTTGCGAGCCACCAT 1380
DB 1081 TTTAGGACTTTTATCAATCTTCTACTTTTACGATTTATTAACAGAACTTTGCGAGCCACCA 1140
QY 1381 TTTTAAATTAACGTTGGTGAAGAGTAGAATTTTCTTACACCTTACAAATAGCTTTACGTAT 1440
DB 1141 TTTTAAATTAACGTTGGTGAAGAGTAGAATTTTCTTACACCTTACAAATAGCTTTACGTAT 1200
QY 1441 GCAGGAAGAGGTACGGTTGATTTTAACTGAAATACCCCTGAGGATTAATAGTGTGCCA 1500
DB 1201 CGAGGAAGAGGTACGGTTGATTTTAACTGAAATACCCCTGAGGATTAATAGTGTGCCA 1260
QY 1501 CTTGCGGAAGGATATAGTCAATCGTTTATGTCATGCAACTTTTGTTCAAAGATCTGGAACA 1560
DB 1261 CTTGCGGAAGGATATAGTCAATCGTTTATGTCATGCAACTTTTGTTCAAAGATCTGGAACA 1320
QY 1561 CTTTGTTTTAAACAACCTGTTGTAGTATTTCTTGGAGCGCATCGTAGTGCACATCTTACAAAT 1620
DB 1321 CTTTGTTTTAAACAACCTGTTGTAGTATTTCTTGGAGCGCATCGTAGTGCACATCTTACAAAT 1380
QY 1621 ACAATTGATCCAGAGAGAAATTAATCAAAATACCTTTTAGTGAAGGATTTAGAGTTTGGGG 1680
DB 1381 ACAATTGATCCAGAGAGAAATTAATCAAAATACCTTTTAGTGAAGGATTTAGAGTTTGGGG 1440
QY 1681 GGCACCTCTGTCTATTAACAGGACCGAGTTTACAGGAGGGAATATCTTTCGAAGAAATACC 1740
DB 1441 GGCACCTCTGTCTATTAACAGGACCGAGTTTACAGGAGGGAATATCTTTCGAAGAAATACC 1500
QY 1741 TTTTGTGATTTTGTATCTCTCAAGTCAATATTAATTTACCAATTTACCCAAAGATACCCGT 1800
DB 1501 TTTTGTGATTTTGTATCTCTCAAGTCAATATTAATTTACCAATTTACCCAAAGATACCCGT 1560
QY 1801 TTAAGATTTTGTAGCTTCCAGTAGGATGACAGATTTATAGTATTAACAGAGCGGCA 1860
DB 1561 TTAAGATTTTGTAGCTTCCAGTAGGATGACAGATTTATAGTATTAACAGAGCGGCA 1620
QY 1861 TCACAGAGGTGGGAGGCGCAAGTTAGTGTAGATATGCTCTTTTCAGAAAATCTATGGAATA 1920
DB 1621 TCACAGAGGTGGGAGGCGCAAGTTAGTGTAGATATGCTCTTTTCAGAAAATCTATGGAATA 1680
QY 1921 GGGGAGAACTTAACTCTAGAACATTTAGATATACCGATTTTAGTAAATCTTTTTCATTT 1980
DB 1681 GGGGAGAACTTAACTCTAGAACATTTAGATATACCGATTTTAGTAAATCTTTTTCATTT 1740
QY 1981 AGAGCTAATCCAGATATTAATTTGGGATAAGTGAAACCACTCTATTTTGGTGCAGGTTCTATT 2040
DB 1741 AGAGCTAATCCAGATATTAATTTGGGATAAGTGAAACCACTCTATTTTGGTGCAGGTTCTATT 1800
QY 2041 AGTAGCGTTGAATTTTATATAGATAAAATTTGAAATTTTCTTAGCAGATGCAACATTTGAA 2100

Db	1801	AGTAGCGGTGAACCTTATATATAGATAAAATTGAATTATTCTACAGATGCAACATTGAA	1860	XX	21-JUN-1999;	99US-0337635.
Qy	2101	GCAGATCTGATTAGAAAGAGCACAAGGCGGTGAATGCGCTGTTACTTCTTCCAAT	2160	XX	26-NOV-1997;	97US-0980071.
Db	1861	GCAGATCTGATTAGAAAGAGCACAAGGCGGTGAATGCGCTGTTACTTCTTCCAAT	1920	PR	27-NOV-1996;	96US-0757536.
Qy	2161	CAATCGGGTAAAAACCGATGTGACGGATTATCATATTGATCAAGTATCCAAATTAGTG	2220	XX	(MONS)	MONSANTO TECHNOLOGY LLC.
Db	1921	CAATCGGGTAAAAACCGATGTGACGGATTATCATATTGATCAAGTATCCAAATTAGTG	1980	XX	Baum JA,	Gilmer AJ, Mettuss AL;
Qy	2221	GATTGTTTATCAGATCAATTTTGTCTGGATGAAAGCGAGAAATGTCCGAGAAAGTCAA	2280	XX	WPI;	2002-033341/04.
Db	1981	GATTGTTTATCAGATCAATTTTGTCTGGATGAAAGCGAGAAATGTCCGAGAAAGTCAA	2040	XX	P-PSDB;	AAE26465.
Qy	2281	CATCGGAAGCGACTCAGTGATGAGCGGAATTTACTTCAAGATCCAACTTCAGAGGGATC	2340	XX	Transgenic plants,	comprises nucleic acid encoding Cry1C
Db	2041	CATCGGAAGCGACTCAGTGATGAGCGGAATTTACTTCAAGATCCAACTTCAGAGGGATC	2100	XX	delta-endotoxin polypeptide,	has improved resistance to Lepidopteran insects
Qy	2341	AAATAGCAACACGACCGTGGCTGGAGAGGAAGTACAGATATTACCATCAAGGAGAGAT	2400	XX	Disclosure;	Column 201-210; 151pp; English.
Db	2101	AAATAGCAACACGACCGTGGCTGGAGAGGAAGTACAGATATTACCATCAAGGAGAGAT	2160	XX	The present invention relates to novel transgenic plants comprising Cry1	delta-endotoxin genes, in particular cry1C genes that encode modified
Qy	2401	GACGTATTCAACAGAAATTAAGTCACTACCGGTACCGTTGATGAGTGCTATCCAAAG	2460	CC	crystal proteins having improved resistance to lepidopteran insects. The	crystal proteins having improved resistance to lepidopteran insects. The
Db	2161	GACGTATTCAACAGAAATTAAGTCACTACCGGTACCGTTGATGAGTGCTATCCAAAG	2220	CC	plants that express the mutated Cry1C delta-endotoxin crystal proteins	are monocotyledonous (corn, wheat, oat, rice, barley, turf grass, pasture
Qy	2461	FATTTATATCAGAAATAGATGAGTCCGAATTTAAAGCTTTATACCGTTATGAAATTAAGA	2520	CC	grasses) or dicotyledonous (legume, soybean, cotton, fruit, berry, tree).	The present sequence is Bacillus thuringiensis Cry1C.499 mutant DNA.
Db	2221	FATTTATATCAGAAATAGATGAGTCCGAATTTAAAGCTTTATACCGTTATGAAATTAAGA	2280	XX	Sequence 3567 BP; 1167 A; 599 C; 791 G; 1010 T; 0 other;	
Qy	2521	GGGTATATCAGAAATAGATGAGTCCGAATTTAAAGCTTTATACCGTTATGAAATTAAGA	2580	XX	Query Match	89.6%; Score 2429.4; DB 24; Length 3567;
Db	2281	GGGTATATCAGAAATAGATGAGTCCGAATTTAAAGCTTTATACCGTTATGAAATTAAGA	2340	XX	Best Local Similarity	98.9%; Pred. No. 0;
Qy	2581	GAAATAGTAATGTGCGAGCGGTCTTATGCGCTTTCAGCCCAAGATCCCAATC	2640	XX	Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;	
Db	2341	GAAATAGTAATGTGCGAGCGGTCTTATGCGCTTTCAGCCCAAGATCCCAATC	2400	Qy	241	ATGAGAGAAATAATCAAAATCAATGATACCTTCAATTTAGTATCTCTCAAGAA 300
Qy	2641	GGAAAGTGTGAGAACGAAATCGATGCGCGCACCTTGATGGAATCTGATCTAGAT	2700	Db	1	ATGAGAGAAATAATCAAAATCAATGATACCTTCAATTTAGTATCTCTCAAGAA 60
Db	2401	GGAAAGTGTGAGAACGAAATCGATGCGCGCACCTTGATGGAATCTGATCTAGAT	2460	Qy	301	GTACTTTTGTGATGAGAGACGGATATCACTGTGTAATTAATCAATGATTTCTCTCA 360
Qy	2701	TGTTCTGCGAG 2711		Db	61	GTACTTTTGTGATGAGAGACGGATATCACTGTGTAATTAATCAATGATTTCTCTCA 120
Db	2461	TGTTCTGCGAG 2471		Qy	361	CTTGTTTCAGTTCTCTGATCTAATCTTTGTACAGGGGAGGATTTTGTGATGATATA 420
				Db	121	CTTGTTTCAGTTCTCTGATCTAATCTTTGTACAGGGGAGGATTTTGTGATGATATA 180
				Qy	421	GATTTTGTATGGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTGAA 480
				Db	181	GATTTTGTATGGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTGAA 240
				Qy	481	CAATTAATTAATGAAAGAAATAGCTGAATTTGTCTAGGAATGCTGCTATTGCTAATTTAGAA 540
				Db	241	CAATTAATTAATGAAAGAAATAGCTGAATTTGTCTAGGAATGCTGCTATTGCTAATTTAGAA 300
				Qy	541	GGATTAGGAACAATTTCAATATATATGTGGAAGCAATTTAAAGAAATCGGAAGATCTCT 600
				Db	301	GGATTAGGAACAATTTCAATATATATGTGGAAGCAATTTAAAGAAATCGGAAGATCTCT 360
				Qy	601	AAATATCAGCAACACGAGGACAGAGTAAATGATGCGCTTTTCGTATACCTTTTATCGGCTACTT 660
				Db	361	CAATATCCAGCAACACGAGGACAGAGTAAATGATGCGCTTTTCGTATACCTTTTATCGGCTACTT 420
				Qy	661	GAAGGGACATCTCTGTTTCGAATTTTCGAATTTGAAATGTAACCTTTTATCGGCTACTT 720
				Db	421	GAAGGGACATCTCTGTTTCGAATTTTCGAATTTGAAATGTAACCTTTTATCGGCTACTT 480
				Qy	721	GCTCAAGCGGCAATCTGATCTAGCTATATTAAGAGATTTCTGTAATTTTGGAGAAAGA 780
				Db	481	GCTCAAGCGGCAATCTGATCTAGCTATATTAAGAGATTTCTGTAATTTTGGAGAAAGA 540
				Qy	781	TTGGGATTTGACACGATTAATGTCGAATGTAACCTTAATAGACTTAATAGACTTAATAGCATATTGAT 840
				Db	541	TGGGGATTTGACACGATTAATGTCGAATGTAACCTTAATAGACTTAATAGACTTAATAGCATATTGAT 600

QY 841 GAATATGCTGATCACTGTGCAAAATACGTAATAATCGGGGATTAATAATTTACCGAAATCT 900
DB 601 GAATATGCTGATCACTGTGCAAAATACGTAATAATCGGGGATTAATAATTTACCGAAATCT 960
QY 901 ACCTATCAAGATTGGATTAACATATAATCGGATTAACGAGAGACATTAACATTTGACGTGATTA 960
DB 661 ACCTATCAAGATTGGATTAACATATAATCGGATTAACGAGAGACATTAACATTTGACGTGATTA 720
QY 961 GATATCGCGCTTTCTTTCCAAACTATGACAAATAGGAGATATCCAAATTCAGCGAGTTGGT 1020
DB 721 GATATCGCGCTTTCTTTCCAAACTATGACAAATAGGAGATATCCAAATTCAGCGAGTTGGT 780
QY 1021 CAATTAACAGGAGATTTATACGGACCCATTAATTAATTTAATCCAGTTACAGTCT 1080
DB 781 CAATTAACAGGAGATTTATACGGACCCATTAATTAATTTAATCCAGTTACAGTCT 840
QY 1081 GTAGCTCAATTTACTCTTTTAAAGTTATGAGAGAGAGCGCAATTAAGAAATCCTCAATTTA 1140
DB 841 GTAGCTCAATTTACTCTTTTAAAGTTATGAGAGAGAGCGCAATTAAGAAATCCTCAATTTA 900
QY 1141 TTTGATATATGTAATCTTACAAATCTTTTACGGATTTGGTTAGTGTGAGCGCAATTTT 1200
DB 901 TTTGATATATGTAATCTTACAAATCTTTTACGGATTTGGTTAGTGTGAGCGCAATTTT 960
QY 1201 TATTGGGAGGACATCGAGTAATATCTAGCTTTATAGGAGTGTGTAACATATCTCT 1260
DB 961 TATTGGGAGGACATCGAGTAATATCTAGCTTTATAGGAGTGTGTAACATATCTCT 1020
QY 1261 ATATATGGAAGAGAGCGGACAGGAGCTTCCAAAGATCCTTTACTTTTAAATGAGCGGTA 1320
DB 1021 ATATATGGAAGAGAGCGGACAGGAGCTTCCAAAGATCCTTTACTTTTAAATGAGCGGTA 1080
QY 1321 TTTAGGACTTTATCAATCTTCTTACGATTTATACAGCAACCTTTGCCAGCGCCACCAT 1380
DB 1081 TTTAGGACTTTATCAATCTTCTTACGATTTATACAGCAACCTTTGCCAGCGCCACCA 1140
QY 1381 TTTAATTTACGTTGGTGAAGAGTAGAATTTTCTACACCTTACAAATAGCTTTAGTAT 1440
DB 1141 TTTAATTTACGTTGGTGAAGAGTAGAATTTTCTACACCTTACAAATAGCTTTAGTAT 1200
QY 1441 GCAGGAAGAGGTACGTTGATCTTTAACTGTAATTTACCGCTTACGAGTAATAGTGTGCA 1500
DB 1201 CGAGGAAGAGGTACGTTGATCTTTTACTGTAATTTACCGCTTACGAGTAATAGTGTGCA 1260
QY 1501 CTTCCGGAAGGATATAGTATCATCGTTTATGTCGCAACTTTTGTTCGAAAGATCTGGAACA 1560
DB 1261 CTTCCGGAAGGATATAGTATCATCGTTTATGTCGCAACTTTTGTTCGAAAGATCTGGAACA 1320
QY 1561 CTTTCTTTTAACTAGCTGTAGTATTTCTTGGACGATCGTAGTGAACCTCTTACAAAT 1620
DB 1321 CTTTCTTTTAACTAGCTGTAGTATTTCTTGGACGATCGTAGTGAACCTCTTACAAAT 1380
QY 1621 ACAATTTGATCCAGAGAGATTAATCAATACCTTTTGTGAAAGGATTTAGTGTGGGG 1680
DB 1381 ACAATTTGATCCAGAGAGATTAATCAATACCTTTTGTGAAAGGATTTAGTGTGGGG 1440
QY 1681 GGCACCTCTGTCTATACAGGACAGGATTTTACAGGAGGGATATCTTCCGAAAGATATACC 1740
DB 1441 GGCACCTCTGTCTATACAGGACAGGATTTTACAGGAGGGATATCTTCCGAAAGATATACC 1500
QY 1741 TTTTGTGATTTTGTATCTCTACAAAGTCAATATAATTTCAACCAATACCAAGATACCGT 1800
DB 1501 TTTTGTGATTTTGTATCTCTACAAAGTCAATATAATTTCAACCAATACCAAGATACCGT 1560
QY 1801 TTAAGATTTTGTATCGTCTTCCAGTGGGATGACAGGATTTATAGTATTAACAGGAGGCA 1860
DB 1561 TTAAGATTTTGTATCGTCTTCCAGTGGGATGACAGGATTTATAGTATTAACAGGAGGCA 1620
QY 1861 TCCACAGGAGTGGGAGGCGCAAGTGTAGTATGCTCTTTCAGAAACTATGGAATA 1920
DB 1621 TCCACAGGAGTGGGAGGCGCAAGTGTAGTATGCTCTTTCAGAAACTATGGAATA 1680
QY 1921 GGGGAGAACTTAACATCTTAGAACAATTTAGATATACCGATTTTGTAGTATCTTTTCAATTT 1980

DB 1681 GGGGAGAACTTAACATCTTAGAACAATTTAGATATACCGATTTTGTAGTATCTTTTCAATTT 1740
QY 1981 AGAGCTTAATCCAGATATATTAATTTGGGATTAAGTGAACAACCTCTTATTTGGTGCAGGTTCTATT 2040
DB 1741 AGAGCTTAATCCAGATATATTAATTTGGGATTAAGTGAACAACCTCTTATTTGGTGCAGGTTCTATT 1800
QY 2041 AGTAGCGTTGAACCTTTATATATAGATAAAATTTGAAAATTTTCTAGCAGATGCAACATTTGAA 2100
DB 1801 AGTAGCGTGAACCTTTATATATAGATAAAATTTGAAAATTTTCTAGCAGATGCAACATTTGAA 1860
QY 2101 GCAGAAATCTGATTTAGAAAGAGCAAAAAGGCGGTGAATGCGCTTGTACTTCTTCCAAAT 2160
DB 1861 GCAGAAATCTGATTTAGAAAGAGCAAAAAGGCGGTGAATGCGCTTGTACTTCTTCCAAAT 1920
QY 2161 CAAATCGGCTTAAACACCGATGTCGCGATTTATCATATTTGATCAAGTATCCAAATTTAGTG 2220
DB 1921 CAAATCGGCTTAAACACCGATGTCGCGATTTATCATATTTGATCAAGTATCCAAATTTAGTG 1980
QY 2221 GATTTCTTTATCAGATGAATTTTGTCTGATGAAAACGAGAAATTTGTCGAGAAAGTCAAA 2280
DB 1981 GATTTCTTTATCAGATGAATTTTGTCTGATGAAAACGAGAAATTTGTCGAGAAAGTCAAA 2040
QY 2281 CATGCGAAGCGACTCAGTGATGAGCGGAATTTTACTTCAAGATCCAAACTTTCAGAGGGATC 2340
DB 2041 CATGCGAAGCGACTCAGTGATGAGCGGAATTTTACTTCAAGATCCAAACTTTCAGAGGGATC 2100
QY 2341 AATAGACAACAGACCGCTGCTGGAGAGGAGTACAGATATTTACCATCCAGGAGAGAT 2400
DB 2101 AATAGACAACAGACCGCTGCTGGAGAGGAGTACAGATATTTACCATCCAGGAGAGAT 2160
QY 2401 GACGTATTTCAAAGAGAAATTTAGCTCACACTACCGGTACCGTTGTAGTGTCTATCCAAAG 2460
DB 2161 GACGTATTTCAAAGAGAAATTTAGCTCACACTACCGGTACCGTTGTAGTGTCTATCCAAAG 2220
QY 2461 TATTTATATCAGAAATAGATGAGTFCGAAATTTAAAGCTTTATACCCGTTATGAATTAAGA 2520
DB 2221 TATTTATATCAGAAATAGATGAGTFCGAAATTTAAAGCTTTATACCCGTTATGAATTAAGA 2280
QY 2521 GGGTATATCGAAGATAGTCAAGACTTGAAGAAATCTTATTTGATCGGTCAATGCAAAACAC 2580
DB 2281 GGGTATATCGAAGATAGTCAAGACTTGAAGAAATCTTATTTGATCGGTCAATGCAAAACAC 2340
QY 2581 GAAATAGTAAATGTGCCAGGACCGGTTCTTTATGGCGCTTTTACGCCAAAAGTCCAATC 2640
DB 2341 GAAATAGTAAATGTGCCAGGACCGGTTCTTTATGGCGCTTTTACGCCAAAAGTCCAATC 2400
QY 2641 GGAAGTGTGAGAAACCGAATCGATGCGCGCCACACCTTTGAATGGAATCTCTGATCTAGAT 2700
DB 2401 GGAAGTGTGAGAAACCGAATCGATGCGCGCCACACCTTTGAATGGAATCTCTGATCTAGAT 2460
QY 2701 TGTTCCTGCAG 2711
DB 2461 TGTTCCTGCAG 2471

RESULT 15

ABS70781
ID ABS70781 standard; DNA; 3567 BP.

XX ABS70781;

XX AC

XX 26-NOV-2002 (first entry)

XX B. thuringiensis DNA encoding CRY mutant Cry1C-R148A.

XX Crystal protein; Cry1C; ds; gene; mutant; delta-endotoxin; insecticide;

XX lepidopteran insect.

XX Bacillus thuringiensis.

XX Synthetic.

XX US6423828-B1.

XX 23-JUL-2002.
 XX 22-JUN-1999; 99US-0337280.
 XX 26-NOV-1997; 97US-0980071.
 XX 27-NOV-1996; 96US-0757536.
 XX (MONS) MONSANTO TECHNOLOGY LLC.
 XX Baum JA, Gilmer AJ, Mettuss AL;
 XX WPI: 2002-705183/76.
 XX P-PSDB; ABG93814.
 XX New delta endotoxin polypeptides, which are Lepidopteran-toxic
 XX polypeptides, useful as an insecticide, particularly for killing
 XX lepidopteran insects or insect cells -
 XX Example 6; Column 105-108; 149pp; English.
 XX The invention relates to an isolated CryIcA* delta-endotoxin polypeptide
 XX useful as an insecticide. CryI is a crystal protein from *B. thuringiensis*.
 XX The isolated CryIcA* delta-endotoxin polypeptide comprises:
 XX (a) one or more amino acid mutations in the loop regions between alpha
 XX helices 4 and 5 of domain 1; (b) one or more amino acid mutations in the
 XX loop region between alpha helices 6 and 7 of domain 1; or (c) has
 XX improved activity against lepidopteran insects relative to a native CryIc
 XX delta-endotoxin polypeptide. The CryIcA* delta-endotoxin polypeptide is
 XX useful as an insecticide, particularly for killing lepidopteran insects
 XX or insect cells. The present sequence encodes a mutant CryIc protein of
 XX the invention.
 XX SQ Sequence 3567 BP; 1168 A; 597 C; 791 G; 1011 T; 0 other;

Query Match 89.6%; Score 2429,4; DB 24; Length 3567;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 241 ATGGAGGAATATCAAAATCAATGCATACCTTACAAATGTTTAACTAATCTGAAGAA 300
 DB 1 ATGGAGGAATATCAAAATCAATGCATACCTTACAAATGTTTAACTAATCTGAAGAA 60
 QY 301 GTACTTTGGATGGAGACGGATCACTGTAATTAATCAATGATATTTCTCTGTCA 360
 DB 61 GTACTTTGGATGGAGACGGATCACTGTAATTAATCAATGATATTTCTCTGTCA 120
 QY 361 CTGTGTCAGTTCTGTTATCTAACTTTGTACACGGGGAGGATTTTGTGGAATATA 420
 DB 121 CTGTGTCAGTTCTGTTATCTAACTTTGTACACGGGGAGGATTTTGTGGAATATA 180
 QY 421 GATTTTGTATGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATGAA 480
 DB 181 GATTTTGTATGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATGAA 240
 QY 481 CAATTAATTAATGAAGAATAGCTGAATTTGCTAGGAATGCTGTATTTAGTAAATTTAGAA 540
 DB 241 CAATTAATTAATGAAGAATAGCTGAATTTGCTAGGAATGCTGTATTTAGTAAATTTAGAA 300
 QY 541 GGATTTAGGAACAAATTTCAATATATGTGGAAGCAATTTAAAGATGGGAAGATCTT 600
 DB 301 GGATTTAGGAACAAATTTCAATATATGTGGAAGCAATTTAAAGATGGGAAGATCTT 360
 QY 601 AATATCCAGCACCGACGAGTAATGATCGCTTTCTGTACTTGTATGATGGCTACTT 660
 DB 361 AATATCCAGCACCGACGAGTAATGATCGCTTTCTGTACTTGTATGATGGCTACTT 420
 QY 661 GAAGGGACATCTCTGTTTCAATTTCTGGATTTGAAGTACCCCTTTATCGGTTAT 720
 DB 421 GAAGGGACATCTCTGTTTCAATTTCTGGATTTGAAGTACCCCTTTATCGGTTAT 480
 QY 721 GCTCAAGCGGCAATCTGCACTATATTAAGAGATCTGTAATTTTGGAGGAAGA 780
 DB 1561 TTAGAGTTTGGTACCGCTTCCAGTAGGATGCACGAGTTTATAGTATTAAACAGGAGCGCA 1620

481 GCTCAAGCGGCAATCTGCACTATATTAAGAGATCTGTAATTTTGGAGGAAGA 540
 QY 781 TTGGATTTGACAAACGATTAATGCTCAATGAAAATTAATAGACTTAATAGGCATATTGAT 840
 DB 541 TGGGATTTGACAAACGATTAATGCTCAATGAAAATTAATAGACTTAATAGGCATATTGAT 600
 QY 841 GAATATGCTGATCACTGTGCAAAATGATTAATCGGGATTAATTAATTTACGGAATCT 900
 DB 601 GAATATGCTGATCACTGTGCAAAATGATTAATCGGGATTAATTAATTTACGGAATCT 660
 QY 901 ACGTATCAAGATTTGGATAACATATAATCGATTACGGAGAGACTTTAACTATGATTA 960
 DB 661 ACGTATCAAGATTTGGATAACATATAATCGATTACGGAGAGACTTTAACTATGATTA 720
 QY 961 GATATCGCGCTTTCTTTCCAAACTATGCAATAGGAGATATCCAATTCAGCCAGTTGGT 1020
 DB 721 GATATCGCGCTTTCTTTCCAAACTATGCAATAGGAGATATCCAATTCAGCCAGTTGGT 780
 QY 1021 CAACTAACAGGAGGAGTTTATACGGACCCCAATTAATTTTAAATCCACAGTTTACAGTCT 1080
 DB 781 CAACTAACAGGAGGAGTTTATACGGACCCCAATTAATTTTAAATCCACAGTTTACAGTCT 840
 QY 1081 GTAGCTCAATACCTACTTTTAACTTATGGAGACGCGCAATTTAGAAATCTCATTTA 1140
 DB 841 GTAGCTCAATACCTACTTTTAACTTATGGAGACGCGCAATTTAGAAATCTCATTTA 900
 QY 1141 TTTGATATTAATTAATCTTACAACTTTACGATTTACGATTTAGGAGACGCGCAATTTAGAAATCT 1200
 DB 901 TTTGATATTAATTAATCTTACAACTTTACGATTTACGATTTAGGAGACGCGCAATTT 960
 QY 1201 TATTTGGGAGACATCGAGTAAATATCTAGCCTTATAGGAGTGTGTAAATACATCTCTCT 1260
 DB 961 TATTTGGGAGACATCGAGTAAATATCTAGCCTTATAGGAGTGTGTAAATACATCTCTCT 1020
 QY 1261 ATATATGGAAGAGAGCGGAACAGGAGCCTTCCAAATCTTCTTACTTTTAAATGGACCGGTA 1320
 DB 1021 ATATATGGAAGAGAGCGGAACAGGAGCCTTCCAAATCTTCTTACTTTTAAATGGACCGGTA 1080
 QY 1321 TTTTAGGACTTTTATCAATTTCTTACTTTTACGATTTATACAGCAACTTCCAGCAGCCACCAT 1380
 DB 1081 TTTTAGGACTTTTATCAATTTCTTACTTTTACGATTTATACAGCAACTTCCAGCAGCCACCAT 1140
 QY 1381 TTTTAAATTTACGTTGGTGAAGAGTAGAATTTTCTTAACTGAATACCGCTGAGGATTAATAGTGCCA 1440
 DB 1141 TTTTAAATTTACGTTGGTGAAGAGTAGAATTTTCTTAACTGAATACCGCTGAGGATTAATAGTGCCA 1200
 QY 1441 CGAGGAAGAGTAGACGTTGATTTCTTAACTGAATACCGCTGAGGATTAATAGTGCCA 1500
 DB 1201 CGAGGAAGAGTAGACGTTGATTTCTTAACTGAATACCGCTGAGGATTAATAGTGCCA 1260
 QY 1501 CCTCGGAAGGATATAGTACGTTTATGTCGAACTTTTGTTCGAAGATCTGGAACA 1560
 DB 1261 CCTCGGAAGGATATAGTACGTTTATGTCGAACTTTTGTTCGAAGATCTGGAACA 1320
 QY 1561 CTTTTTTTAACTGCTGTTGATTAATTTCTTGGACGATCGTAGTGCAACTCTTACAAAT 1620
 DB 1321 CTTTTTTTAACTGCTGTTGATTAATTTCTTGGACGATCGTAGTGCAACTCTTACAAAT 1380
 QY 1621 ACAATTTGATCCAGAGAGAAATTAATCAAAATACCTTTTATAGTGAAGAGATTTAGAGTTTGGGG 1680
 DB 1381 ACAATTTGATCCAGAGAGAAATTAATCAAAATACCTTTTATAGTGAAGAGATTTAGAGTTTGGGG 1440
 QY 1681 GGCACCTCTGCTAATACAGGACAGGATTTTACAGGAGGGGATATCTTTCGAAGAATAATCC 1740
 DB 1441 GGCACCTCTGCTAATACAGGACAGGATTTTACAGGAGGGGATATCTTTCGAAGAATAATCC 1500
 QY 1741 TTTTGTGATTTTGTATCTCTCAAGTCAATTAATTAATTTTACCAATTTACCAAGATACCGT 1800
 DB 1501 TTTTGTGATTTTGTATCTCTCAAGTCAATTAATTAATTTTACCAATTTACCAAGATACCGT 1560
 QY 1801 TTAGAGTTTGGTACCGCTTCCAGTAGGATGCACGAGTTTATAGTATTAAACAGGAGCGCA 1860
 DB 1561 TTAGAGTTTGGTACCGCTTCCAGTAGGATGCACGAGTTTATAGTATTAAACAGGAGCGCA 1620

QY 1861 TCCACAGGAGTGGGAGGCCAAGTTAGTGTAGATATGCTCTTCAGAAAACTATGGAATA 1920
DB |||||
DB 1621 TCCACAGGAGTGGGAGGCCAAGTTAGTGTAAATATGCTCTTCAGAAAACTATGGAATA 1680
QY 1921 GGGGAGAACTTAACATCTAGACATTTAGATACCGATTTAGTAATCCTTTTCATTT 1980
DB |||||
DB 1681 GGGGAGAACTTAACATCTAGACATTTAGATACCGATTTAGTAATCCTTTTCATTT 1740
QY 1981 AGAGCTAATCCAGATATAATTTGGGATAAGTGAACAACTCTATTGGTCAGGTTCTATT 2040
DB |||||
DB 1741 AGAGCTAATCCAGATATAATTTGGGATAAGTGAACAACTCTATTGGTCAGGTTCTATT 1800
QY 2041 AGTAGCGTTGAACCTTTATATAGATAAAATTTGAAATTTATTCTAGCAGATGCAACATTTGAA 2100
DB |||||
DB 1801 AGTAGCGTTGAACCTTTATATAGATAAAATTTGAAATTTATTCTAGCAGATGCAACATTTGAA 1860
QY 2101 GCAGAACTCTGATTTAGAAAGAGCACAAAGGGCGTGAATGCCCTGTTTACTTCTCCAAAT 2160
DB |||||
DB 1861 GCAGAACTCTGATTTAGAAAGAGCACAAAGGGCGTGAATGCCCTGTTTACTTCTCCAAAT 1920
QY 2161 CAAATCGGTTAAAAACCGATGTGACGGATTTATCATATTGATCAAGTATCCAAATTTAGTG 2220
DB |||||
DB 1921 CAAATCGGTTAAAAACCGATGTGACGGATTTATCATATTGATCAAGTATCCAAATTTAGTG 1980
QY 2221 GATTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGAGAAATGTCCGAGAAAGTCAAA 2280
DB |||||
DB 1981 GATTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGAGAAATGTCCGAGAAAGTCAAA 2040
QY 2281 CATGCGAAGCGACTGATGATGAGCGGAATTTACTTCAAGATCCAACTTCAGAGGGATC 2340
DB |||||
DB 2041 CATGCGAAGCGACTGATGATGAGCGGAATTTACTTCAAGATCCAACTTCAGAGGGATC 2100
QY 2341 AATAGACAACCGACCGTGGCTGGAGAGGATGACAGATATTACCATCCAAGGAGGAGAT 2400
DB |||||
DB 2101 AATAGACAACCGACCGTGGCTGGAGAGGATGACAGATATTACCATCCAAGGAGGAGAT 2160
QY 2401 GACGTATTCAAAGAGAAATACGTCACTACCGGGTACCGTTGATGAGTGCTATCCAACG 2460
DB |||||
DB 2161 GACGTATTCAAAGAGAAATACGTCACTACCGGGTACCGTTGATGAGTGCTATCCAACG 2220
QY 2461 TATTTATATCAGAAATAGATGATGCTGAAATTTAAAGCTTTATACCGTTATGAATTAAGA 2520
DB |||||
DB 2221 TATTTATATCAGAAATAGATGATGCTGAAATTTAAAGCTTTATACCGTTATGAATTAAGA 2280
QY 2521 GGGTATATCGAAGATAGTCAAGACTTGAATAATCTATTGATCGCGTACAAATGCAAAACAC 2580
DB |||||
DB 2281 GGGTATATCGAAGATAGTCAAGACTTGAATAATCTATTGATCGGTACANTGCAAAACAC 2340
QY 2581 GAAATAGTAAATGTGCCAGCACGGGTTCCTTTATGCGCGCTTTACGCCCAAAAGTCCAATC 2640
DB |||||
DB 2341 GAAATAGTAAATGTGCCAGCACGGGTTCCTTTATGCGCGCTTTACGCCCAAAAGTCCAATC 2400
QY 2641 GGAAGTGTGGAGAACCGAATGATGCGGCCACACCTTTGAATGGAATCCTGATCTAGAT 2700
DB |||||
DB 2401 GGAAGTGTGGAGAACCGAATGATGCGGCCACACCTTTGAATGGAATCCTGATCTAGAT 2460
QY 2701 TGTTCCTGCAG 2711
DB |||||
DB 2461 TGTTCCTGCAG 2471

Search completed: October 13, 2003, 04:44:44
Job time : 869 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: October 13, 2003, 03:40:26 ; Search time 12714 Seconds
(without alignments)
8723.140 Million cell updates/sec

Title: US-09-918-485-1
Perfect score: 2711
Sequence: 1 AGCTTCATAGAACTCAA.....GATCTAGATTGTCCTGCAG 2711

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_cm.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sta.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
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22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sta.*
28: em_un.*
29: em_vi.*
30: em_hgt_hum.*
31: em_hgt_inv.*
32: em_hgt_other.*
33: em_hgt_mus.*
34: em_hgt_pln.*
35: em_hgt_rod.*
36: em_hgt_mam.*
37: em_hgt_vrt.*
38: em_sy.*
39: em_hgtgo_hum.*
40: em_hgtgo_mus.*
41: em_hgtgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2711	100.0	2711	6	AR022642	Sequence AR022642
2	2711	100.0	2711	6	ARI75979	Sequence ARI75979
3	2696.6	99.5	2711	1	BTTOXDA	Sequence X13620 Bacillus th
4	2696.2	99.5	2711	6	A00221	Sequence A00221 Nucleotide
5	2696.2	99.5	2711	6	A10218	Sequence A10218 B.thuringie
6	2671.6	98.5	4930	1	AF362020	Sequence AF362020 Bacillus
7	2664	98.3	3903	6	A27642	Sequence A27642 B.thuringie
8	2664	98.3	3923	6	A31099	Sequence A31099 B.thuringie
9	2664	98.3	3923	6	AR032226	Sequence AR032226
10	2659.2	98.1	3923	6	ARI25059	Sequence ARI25059
11	2470.6	91.1	3706	1	BTETOXD	Sequence X07518 Bacillus th
12	2446.6	90.2	3646	1	AY078160	Sequence AY078160 Bacillus
13	2431	89.7	3567	6	A43696	Sequence A43696
14	2431	89.7	3567	6	AR000001	Sequence AR000001
15	2431	89.7	3567	6	ARI43374	Sequence ARI43374
16	2429.4	89.6	3567	6	ARI05485	Sequence ARI05485
17	2429.4	89.6	3567	6	ARI20161	Sequence ARI20161
18	2429.4	89.6	3567	6	ARI20166	Sequence ARI20166
19	2429.4	89.6	3567	6	ARI26159	Sequence ARI26159
20	2429.4	89.6	3567	6	ARI26164	Sequence ARI26164
21	2429.4	89.6	3567	6	ARI77975	Sequence ARI77975
22	2429.4	89.6	3567	6	ARI77980	Sequence ARI77980
23	2429.4	89.6	3567	6	AR220279	Sequence AR220279
24	2429.4	89.6	3567	6	AR220284	Sequence AR220284
25	2429.4	89.6	3567	6	BD063749	Sequence BD063749 DNA encod
26	2429.4	89.6	3567	6	BD063754	Sequence BD063754 DNA encod
27	2429.4	89.6	3567	6	I76416	Sequence I76416
28	2429.4	89.6	3570	1	BACCRYICB	Sequence M73251 Bacillus th
29	2427.8	89.6	3567	6	ARI20162	Sequence ARI20162
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38	2427.8	89.6	3567	6	AR220280	Sequence AR220280
39	2427.8	89.6	3567	6	AR220281	Sequence AR220281
40	2427.8	89.6	3567	6	AR220283	Sequence AR220283
41	2427.8	89.6	3567	6	BD063750	Sequence BD063750 DNA encod
42	2427.8	89.6	3567	6	BD063751	Sequence BD063751 DNA encod
43	2427.8	89.6	3567	6	BD063753	Sequence BD063753 DNA encod
44	2427.8	89.6	3570	1	AF215647	Sequence AF215647
45	2426.2	89.5	3567	6	ARI20164	Sequence ARI20164

ALIGNMENTS

RESULT 1
AR022642
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

AR022642
Sequence 1 from patent US 5792928.
AR022642
AR022642.1 GI:3976704
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 2711)
Sanchis,V., Lereclus,D., Menou,G., Lecadet,M.-M., Martouret,D. and
Dedonder,R.
Nucleotide sequences coding for polypeptides endowed with a
larvicidal activity towards lepidoptera

linear PAT 05-DEC-1998

JOURNAL Patent: US 5792928-A 1 11-AUG-1998;

FEATURES Location/Qualifiers

1..2711 /organism="unknown"

BASE COUNT 879 a 442 c 556 g 834 t

ORIGIN

Query Match 100.0%; Score 2711; DB 6; Length 2711;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AAGCTTCAATAGAACTCTCAAACTCTCGATGACTGCTTACTCTTTTAAATAGTCTACTTG 60

1 AAGCTTCAATAGAACTCTCAAACTCTCGATGACTGCTTACTCTTTTAAATAGTCTACTTG 60

61 ACAGGGGTAGAACATTAATCGGTCAATTTTAAATATGGGCATATATTCATATTTTATAA 120

61 ACAGGGGTAGAACATTAATCGGTCAATTTTAAATATGGGCATATATTCATATTTTATAA 120

121 AATTGTGTTAGTCTTTTCTGTTTATTTTTCATAAGATGTGTCATATGATTAATTCGTGTAA 180

121 AATTGTGTTAGTCTTTTCTGTTTATTTTTCATAAGATGTGTCATATGATTAATTCGTGTAA 180

181 TGAATAACAGTATCAAACTATCAGACTTTGGTAGTTTAAATAAAAAACGGAGGTATTTT 240

181 TGAATAACAGTATCAAACTATCAGACTTTGGTAGTTTAAATAAAAAACGGAGGTATTTT 240

241 ATGAGGAAATTAATCAAACTATCAGACTTTGGTAGTTTAAATAAAAAACGGAGGTATTTT 300

241 ATGAGGAAATTAATCAAACTATCAGACTTTGGTAGTTTAAATAAAAAACGGAGGTATTTT 300

301 GPACTTTGATGGGAAATAGTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTTGAA 480

301 GPACTTTGATGGGAAATAGTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTTGAA 480

421 GATTTTGTATGGGAAATAGTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTTGAA 540

421 GATTTTGTATGGGAAATAGTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTTGAA 540

481 CAATTAATTAATGAAAGAAATAGTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTTGAA 540

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541 GGATTAAGAAACAAATTTCAATATATATGTGGAAGCAATTTAAAGATGGGAAAGATCTT 600

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601 AATAATCCAGCAACACGAGCAAGATTAATGATCGCTTTCTGATATACCCCTTTTATCCGTTAT 720

661 GAAAGGGACATTTCTGTTTGGATTTCTGATTTTGAAGTACCCCTTTTATCCGTTAT 720

661 GAAAGGGACATTTCTGTTTGGATTTCTGATTTTGAAGTACCCCTTTTATCCGTTAT 720

721 GCTCAAGGGCAATCTGATCTAGCTATATTAAGATTTCTGATTTTGGGAAAGA 780

721 GCTCAAGGGCAATCTGATCTAGCTATATTAAGATTTCTGATTTTGGGAAAGA 780

781 TTGGGATTCGAAACGATTAATGTCGAACTTAATAGCTAATTAAGCATTTATGAT 840

781 TTGGGATTCGAAACGATTAATGTCGAACTTAATAGCTAATTAAGCATTTATGAT 840

841 GAATATGCTGATCTGCTGCAATGATTAATCGGGATTAATTAATTTCCGAATCT 900

841 GAATATGCTGATCTGCTGCAATGATTAATCGGGATTAATTAATTTCCGAATCT 900

901 ACGTATCAAGATTGATTAACATTAATCGATTAACGAGAGATTAACATTCAGTCTATTA 960

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Qy

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Qy

Db

Qy

Db

Qy

Db

2041 AGTAGCGTTGAACTTTATATAGATATAAATTTGAAATTTATTTCTAGCAGATGCAACATTTGAA 2100
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 2161 CAAATCGGGTTAAAAACCGATGTGACGGATTATCATATTGATCAAGTATCCAAATTTAGTG 2220
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 2221 GATTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGAGAAATTTGTCGCGAAGAAATGCAAA 2280
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 2341 AATAGACAAACAGACCGTGGCTGGAGAGGAAGTACAGATATTACCATCCAAAGGAGAGAT 2400
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 2401 GAGCTATTCAAAGAGAAATTAAGTACACTACCGGGTACCGTTGATGAGTCTATCCAAAG 2460
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 2701 TGTTCCTGCAG 2711
 2701 TGTTCCTGCAG 2711

RESULT 2
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 LOCUS ARI175979 2711 bp DNA linear PAT 17-DEC-2001
 DEFINITION Sequence 1 from patent US 6310035.
 ACCESSION ARI175979
 VERSION ARI175979.1 GI:17917278
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 2711)
 AUTHORS Sanchis,V., Lereclus,D., Menou,G., Lecadet,M.-M., Martouret,D. and Dedonder,R.
 TITLE Polypeptides endowed with a larvicidal activity toward Lepidoptera
 JOURNAL Patent: US 6310035-A 130-OCT-2001;
 FEATURES
 source Location/Qualifiers
 1..2711 /organism="unknown"
 BASE COUNT 879 a 442 c 556 g 834 t
 ORIGIN
 Query Match 100.0%; Score 2711; DB 6; Length 2711;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 2711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 AAGCTTCAATAGAACTCTCAAAATCTCGATGACTGCTTAGTCTCTTTTAAATAGTCTACTTGG 60
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 DB 61 ACAGGGGTAGGAACAATAATCGGTCAATTTTAAATATGCGGCATATATTCATATTTTATAA 120
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 DB 121 AATTTGTTACGTTTTTTGTTATTTTTCATAAGATGTCATATGTTTAAATCGTGGTAA 180
 QY 181 TGAATAACAGTATCAAACTATCAGAACTTTTGTGTAGTTTAAATAAAAACCGAGGTATTTT 240
 DB 181 TGAATAACAGTATCAAACTATCAGAACTTTTGTGTAGTTTAAATAAAAACCGAGGTATTTT 240
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 QY 301 GTACTTTTGGATGGAGAACGGATATCACTGGTGAATTAATCAATGATATTTCTCTGTCA 360
 DB 301 GTACTTTTGGATGGAGAACGGATATCACTGGTGAATTAATCAATGATATTTCTCTGTCA 360
 QY 361 CTTGTTTCAAGTTTCTGGTATCTAACTTTGTACACGAGGAGGATTTTGTAGTGGATTAATA 420
 DB 361 CTTGTTTCAAGTTTCTGGTATCTAACTTTGTACACGAGGAGGATTTTGTAGTGGATTAATA 420
 QY 421 GAATTTGATGCGGAATAGTTGGCCCTTCTCAATGGATGCTATCTAGTACAAATTTGAA 480
 DB 421 GAATTTGATGCGGAATAGTTGGCCCTTCTCAATGGATGCTATCTAGTACAAATTTGAA 480
 QY 481 CAATTAATTAATGAAGAAATAGTCAATTTGCTAGGAATGCTGCTATTTGCTAATTTAGAA 540
 DB 481 CAATTAATTAATGAAGAAATAGTCAATTTGCTAGGAATGCTGCTATTTGCTAATTTAGAA 540
 QY 541 GGATTTAGGAACAATTTCAATATATATGTTGGAAGCAATTTAAAGAAATGGAAGAAATCCT 600
 DB 541 GGATTTAGGAACAATTTCAATATATATGTTGGAAGCAATTTAAAGAAATGGAAGAAATCCT 600
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 DB 601 AATAATCCAGCAACAGGACCCAGAGTAATTTGATCGCTTTTCTGATATCTTGGATGGCTACTT 660
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 DB 661 GAAAGGACATTCCTTCTGTTTTCGAATTTCTGATTTGAAGTACCCCTTTTATCCGTTAT 720
 QY 721 GCTCAAGCGGCAATCTGCTATATTAAGAGATTTCTGTAATTTTTCGAGAAAGA 780
 DB 721 GCTCAAGCGGCAATCTGCTATATTAAGAGATTTCTGTAATTTTTCGAGAAAGA 780
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 QY 841 GAATATGCTGATCCTGTCGAAATACGTATTAATCGGGATTAATAATTTTACCGAAATCT 900
 DB 841 GAATATGCTGATCCTGTCGAAATACGTATTAATCGGGATTAATAATTTTACCGAAATCT 900
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 QY 1021 CAACTAAACAGGGAAGTTTATACGGAACCATTAATTTTAAATTTTAAATCCACAGTTACAGTCT 1080
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QY	1081	GTAGCTCAATTACCTACTTTTAAAGTTATGAGAGACGCGCAATTAGAAATCCTCATTTA	1140
Db	1081	GTAGCTCAATTACCTACTTTTAAAGTTATGAGAGACGCGCAATTAGAAATCCTCATTTA	1140
QY	1141	TTTGATATATGAAATTAATCTTACAACTTTTACGATTTAGGATTTAGTCTGAGCGCAATTTT	1200
Db	1141	TTTGATATATGAAATTAATCTTACAACTTTTACGATTTAGGATTTAGTCTGAGCGCAATTTT	1200
QY	1201	TATTGGGAGGACATCGAGTAATATCTAGCTTTATAGAGTGGTAAATACATCTCTCT	1260
Db	1201	TATTGGGAGGACATCGAGTAATATCTAGCTTTATAGAGTGGTAAATACATCTCTCT	1260
QY	1261	ATATATCGAAGAGGCGCAACAGGAGCCTCCAGATCTTTTAACTTTTATGAGCGGTA	1320
Db	1261	ATATATCGAAGAGGCGCAACAGGAGCCTCCAGATCTTTTAACTTTTATGAGCGGTA	1320
QY	1321	TTTAGGACTTTTAACTTCAATCTTACGATTTATACGATTTATACGAGCGCCACCAT	1380
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QY	1381	TTTAAATTTAGCTGCTGAGGAGTAGAATTTTCTACACCTCAAAATAGCTTTACGTAT	1440
Db	1381	TTTAAATTTAGCTGCTGAGGAGTAGAATTTTCTACACCTCAAAATAGCTTTACGTAT	1440
QY	1441	GCAGAGAGGATACGCTGATTTTAACTGATTTATACGAGCGCTGAGGATTAATAGTGCCA	1500
Db	1441	GCAGAGAGGATACGCTGATTTTAACTGATTTATACGAGCGCTGAGGATTAATAGTGCCA	1500
QY	1501	CCTCGGAGGATATAGTCATCTGTTATGATCATGCAACTTTTGTTCAGAGATCTGGAACA	1560
Db	1501	CCTCGGAGGATATAGTCATCTGTTATGATCATGCAACTTTTGTTCAGAGATCTGGAACA	1560
QY	1561	CTTTTATCAACTGCTGATGATTTTCTGAGCGCATCTGATGCAACTCTTCAAAAT	1620
Db	1561	CTTTTATCAACTGCTGATGATTTTCTGAGCGCATCTGATGCAACTCTTCAAAAT	1620
QY	1621	ACAATGATTCAGAGAAATTAATCAATACCTTTAGTGAAGAGATTTAGAGTTGGGG	1680
Db	1621	ACAATGATTCAGAGAAATTAATCAATACCTTTAGTGAAGAGATTTAGAGTTGGGG	1680
QY	1681	GGCACCCTGCTATTACAGGACAGGATTTACAGAGGGGATATCTTCAAGAAATACC	1740
Db	1681	GGCACCCTGCTATTACAGGACAGGATTTACAGAGGGGATATCTTCAAGAAATACC	1740
QY	1741	TTTGGTGAATTTGATCTCTACAAGTCAATTAATTAATTCACCAATTAACCAAGATACCT	1800
Db	1741	TTTGGTGAATTTGATCTCTACAAGTCAATTAATTAATTCACCAATTAACCAAGATACCT	1800
QY	1801	TTAAGATTTCTGTTACGCTTCCAGTAGGATGCGACGATTTATAGTTAAACAGAGCGCA	1860
Db	1801	TTAAGATTTCTGTTACGCTTCCAGTAGGATGCGACGATTTATAGTTAAACAGAGCGCA	1860
QY	1861	TCCACAGGAGTGGGAGGCGCAAGTTAGTGTAGATATGCTCTTCAGAAACTATGGAATA	1920
Db	1861	TCCACAGGAGTGGGAGGCGCAAGTTAGTGTAGATATGCTCTTCAGAAACTATGGAATA	1920
QY	1921	GGGAGAGCTTAACATCTAGACATTTAGATATACCAATTTAGTAATCTTTTTCATTT	1980
Db	1921	GGGAGAGCTTAACATCTAGACATTTAGATATACCAATTTAGTAATCTTTTTCATTT	1980
QY	1981	AGAGCTATCCAGATATAATTTGGATAGTGAACAACCTCTATTGTTGGTCAAGTTCTATT	2040
Db	1981	AGAGCTATCCAGATATAATTTGGATAGTGAACAACCTCTATTGTTGGTCAAGTTCTATT	2040
QY	2041	AGTAGGTTGAACCTTTATAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2100
Db	2041	AGTAGGTTGAACCTTTATAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2100
QY	2101	GCAGATCTGATTTAGAAAGAGCACAAGAGCGGTGAATGCTGCTTCTTCCCAT	2160
Db	2101	GCAGATCTGATTTAGAAAGAGCACAAGAGCGGTGAATGCTGCTTCTTCTCCCAT	2160
QY	2161	CAATCGGTTTAAAAACCGGATGTGACGGAATTCATATTTGATCAAGTATCCAAATTTAGTG	2220
Db	2161	CAATCGGTTTAAAAACCGGATGTGACGGAATTCATATTTGATCAAGTATCCAAATTTAGTG	2220
QY	2221	GATTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGAAGATTTGTCGAGAAAGTCAAA	2280
Db	2221	GATTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGAAGATTTGTCGAGAAAGTCAAA	2280
QY	2281	CATGCGAAGCGACTCAGTGAATGAGCGGAATTTACTTCAAGATCCAAACTTCAGAGGATC	2340
Db	2281	CATGCGAAGCGACTCAGTGAATGAGCGGAATTTACTTCAAGATCCAAACTTCAGAGGATC	2340
QY	2341	AATAGCAACACAGACCGCTGCTGAGAGAGAGTACAGATTAATACCATCCAAAGGAGAT	2400
Db	2341	AATAGCAACACAGACCGCTGCTGAGAGAGAGTACAGATTAATACCATCCAAAGGAGAT	2400
QY	2401	GAGTATTCAGAGGAATTAACGTACACCTACCGGTACCGTGTAGTGTGCTATCCAAAG	2460
Db	2401	GAGTATTCAGAGGAATTAACGTACACCTACCGGTACCGTGTAGTGTGCTATCCAAAG	2460
QY	2461	TATTTATATCAGAAATAGATGATCGAATTTAAAGCTTATACCGTGTATGAATTAAGA	2520
Db	2461	TATTTATATCAGAAATAGATGATCGAATTTAAAGCTTATACCGTGTATGAATTAAGA	2520
QY	2521	GGGTATATCGAAGATAGTCAAGACTTAGAATCTATTGATCGGTACGAATGCAAAACAC	2580
Db	2521	GGGTATATCGAAGATAGTCAAGACTTAGAATCTATTGATCGGTACGAATGCAAAACAC	2580
QY	2581	GAAATAGTAAATGTCCAGGACGCGGTTCTTTATGCGCGCTTCAGCCCAAGTCCATC	2640
Db	2581	GAAATAGTAAATGTCCAGGACGCGGTTCTTTATGCGCGCTTCAGCCCAAGTCCATC	2640
QY	2641	GGAAAGTGGGAGAACCGAATTCGATCGCGGACACACTTGATGAATGGAATCTGATCTAGAT	2700
Db	2641	GGAAAGTGGGAGAACCGAATTCGATCGCGGACACACTTGATGAATGGAATCTGATCTAGAT	2700
QY	2701	TGTTCTCTGCAG 2711	
Db	2701	TGTTCTCTGCAG 2711	
RESULT 3			
BTTOXDA			
LOCUS		2711 bp	DNA linear BCT 06-JUL-1989
DEFINITION			Bacillus thuringiensis aizawai delta-endotoxin gene 5'-region.
ACCESSION		X13620.1	GI:40355
VERSION			crystal protein; delta-endotoxin; endotoxin; toxin.
KEYWORDS			Bacillus thuringiensis
SOURCE			Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
ORGANISM			
REFERENCE			1 (bases 1 to 2711)
AUTHORS			Sanchis, V., Lereclus, D., Menou, G., Chauvaud, J., Guo, S. and Lecadet, M.M.
TITLE			Nucleotide sequence and analysis of the N-terminal coding region of the Spodoptera-active delta-endotoxin gene of Bacillus thuringiensis aizawai 7,29
JOURNAL			Mol. Microbiol. 3 (2), 229-238 (1989)
MEDLINE			89343627
PUBMED			2548060
REFERENCE			2 (bases 1 to 2711)
AUTHORS			Sanchis, V.
TITLE			Direct Submission
JOURNAL			Submitted (25-NOV-1988) Sanchis V., Institut Pasteur, Unite de Biochimie Microbienne, 25 Rue du Docteur Roux, 75724 Paris Cedex 15, France
COMMENT			See also acc#. x07518.
FEATURES			Data kindly reviewed (10-Apr-1989) by Sanchis V.
SOURCE			1. 2711
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CDS		241..>2711					
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		/transl_table=11					
		/protein_id="CAA31951.1"					
		/db_xref="GI:40356"					
		/translation="MEENNOCIPYNCCLNSPEVLLDGERISTGNSSIDISLIVQF					
		LVSNFVGGFLVLDIFVMGIVGRSOWDAFLVQIEQLINERIAEPARNAUANLEGL					
		GNFNLYVEAFKEMEDPNPATRIVDIRFRILDLGLLDRIDIPSRISGFEPPLISVY					
		AQANJHLAIRDVIFGRWGLTITNVNENYRRIPIQVQGLTREVYTDPLINFP					
		KSTYQWITNRLRDLTLVDIAAFFNNRRIPIQVQGLTREVYTDPLINFP					
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		GNITSPIYGRANOEPRGFPVFTLSIPTLRLLQPCORHFNLRGEGVEFS					
		TPNSFTYGRGTVDLSITLPPEDNSVPREGVSHRLCHATFVQBSGTPLATGVFS					
		WHSATLITDIPERINQIPLVGRFVWGTSVTPGFTGDIILRRNFGDPVSLQ					
		VINSITQIRURFRIASSRDARVILVTGAAGTVGGQVSVNMPKQWIEIGENLTS					
		RTFRYDFSNPFRANPDIIGISEQFLFCAGSISSEELYIDIKIEILADATFEASD					
		LERAQAVNALFTSSNQIGLKTVDYDHIQVSNLVDLSDFCLDEKRELSEKVKHA					
		KRLSDRNLLQPNFRGINKRQDGRWGSTDITIQGGDDVFKENYVTLPLGTWDECVPT					
		YLYOKIDESKLKATYELRGVIEDSDLEIYLIYANAKHEIVNVPGTGSLWPLSAQS					
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BASE COUNT		880 a 442 c 557 g 832 t					
ORIGIN							
Query Match		99.5%; Score 2696.6; DB 1; Length 2711;					
Best Local Similarity		99.7%; Pred. No. 0;					
Matches 2702; Conservative		0; Mismatches 9; Indels 0; Gaps 0;					
QY	1	AAGCTTCAATAGAACTCTCAAACTCGATGACTGCTTTAGTCTTTTAAATAGTCTACTTG	60	QY	541	GGATTAGGAAACAAATTTCAATATATATGTGGAGCAATTTAAAGATGGGAGAAAGATCCT	600
DB	1	AAGCTTCAATAGAACTCTCAAACTCGATGACTGCTTTAGTCTTTTAAATAGTCTACTTG	60	DB	541	GGATTAGGAAACAAATTTCAATATATATGTGGAGCAATTTAAAGATGGGAGAAAGATCCT	600
QY	61	ACAGGGGTAGGAACATAATCGTCAATTTTAAATATGGGCAATATATGATATTTATAA	120	QY	601	AATAATCCAGCAACACGAGGACAGAGTAATTTGATCGCTTTTGGTATCTGATCGGCTACTT	660
DB	61	ACAGGGGTAGGAACATAATCGTCAATTTTAAATATGGGCAATATATGATATTTATAA	120	DB	601	AATAATCCAGCAACACGAGGACAGAGTAATTTGATCGCTTTTGGTATCTGATCGGCTACTT	660
QY	121	AATTGTGACGTTTGTGATTTTTCATAAGATGTGCATATGATTAATTAATCGTGTAA	180	QY	661	GAAGGGAACATTTCTGTTTGGATTTTGAAGTACCCCTTTTATCCGTTTAT	720
DB	121	AATTGTGACGTTTGTGATTTTTCATAAGATGTGCATATGATTAATTAATCGTGTAA	180	DB	661	GAAGGGAACATTTCTGTTTGGATTTTGAAGTACCCCTTTTATCCGTTTAT	720
QY	181	TGAAAAACAGTATCAAACTATCAGAACTTTGGTAGTTTAAATAAAAAACGAGGTATTTT	240	QY	721	GCTCAAGCGGCAATCTGATCTAGCTATATTAAGAGATCTGTAATTTTGGAGAAAGA	780
DB	181	TGAAAAACAGTATCAAACTATCAGAACTTTGGTAGTTTAAATAAAAAACGAGGTATTTT	240	DB	721	GCTCAAGCGGCAATCTGATCTAGCTATATTAAGAGATCTGTAATTTTGGAGAAAGA	780
QY	241	ATGGAGAAATTAATCAAAATCAATGATACCTTCAATGTTTAAAGTAACTCTGAGAA	300	QY	781	TTGGGATTCACACCAAGTAATCTCAATGAAACTATATAGACTAATTAGGCATATTGAT	840
DB	241	ATGGAGAAATTAATCAAAATCAATGATACCTTCAATGTTTAAAGTAACTCTGAGAA	300	DB	781	TTGGGATTCACACCAAGTAATCTCAATGAAACTATATAGACTAATTAGGCATATTGAT	840
QY	301	GTACTTTTGGATGGAGACGATATCAACTGGTAAATTTCAATGATATTTCTGTCTCA	360	QY	841	GAATATGCTGATCCTGTCGAAATAGTATAATCGGGATTTAAATTTTACCGAAATCT	900
DB	301	GTACTTTTGGATGGAGACGATATCAACTGGTAAATTTCAATGATATTTCTGTCTCA	360	DB	841	GAATATGCTGATCCTGTCGAAATAGTATAATCGGGATTTAAATTTTACCGAAATCT	900
QY	361	CTTGTTCAGTTTCTGTTCTAACTTTGTACAGGGGGAGGATTTTGTGTTGATTAATA	420	QY	901	ACGTATCAAGATTTGGATACATATATCGATTCAGGAGAGACTTAACTTGAATTTA	960
DB	361	CTTGTTCAGTTTCTGTTCTAACTTTGTACAGGGGGAGGATTTTGTGTTGATTAATA	420	DB	901	ACGTATCAAGATTTGGATACATATATCGATTCAGGAGAGACTTAACTTGAATTTA	960
QY	421	GATTTTGTATGGGAAATAGTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATGAA	480	QY	961	GATATCGCGCTTTCTTTCCAACTATGCAATAGGAGATATCCAAATTCAGCAGTGGT	1020
DB	421	GATTTTGTATGGGAAATAGTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATGAA	480	DB	961	GATATCGCGCTTTCTTTCCAACTATGCAATAGGAGATATCCAAATTCAGCAGTGGT	1020
QY	481	CAATTAATTAATGAAGAATAGCTGAATTTGCTAGGAATGCTGCTATTTAGTAA	540	QY	1021	CAACTAAACAGGGAAGTTTATACGACCCATTAATTTTAAATCCACAGTTTACAGTCT	1080
DB	481	CAATTAATTAATGAAGAATAGCTGAATTTGCTAGGAATGCTGCTATTTAGTAA	540	DB	1021	CAACTAAACAGGGAAGTTTATACGACCCATTAATTTTAAATCCACAGTTTACAGTCT	1080

Db	1621	ACAATTGATCCAGAGAGAAATTAATCAATACCTTTTGTGGAAGANTTAGATTGGGG	1680
Qy	1681	GGCACTCTGTCTATTACAGACACAGAGATTTACAGAGGGGATATCTCTCGAAGATACC	1740
Db	1681	GGCACTCTGTCTATTACAGACACAGAGATTTACAGAGGGGATATCTCTCGAAGATACC	1740
Qy	1741	TTTGGTGATTTGTATCTCTCAAGTAGTCAATATTAATCAACAATACCCAAAGATACCGT	1800
Db	1741	TTTGGTGATTTGTATCTCTCAAGTAGTCAATATTAATCAACAATACCCAAAGATACCGT	1800
Qy	1801	TTAAGATTTTCGTTAGCTTCCAGTAGGGATGACAGATTTAGTATTAACAGAGCGGCA	1860
Db	1801	TTAAGATTTTCGTTAGCTTCCAGTAGGGATGACAGATTTAGTATTAACAGAGCGGCA	1860
Qy	1861	TCCACAGAGTGGGAGGCGCAAGTTAGTGTAGATATGCTCTTCAGAAAATATGAAATA	1920
Db	1861	TCCACAGAGTGGGAGGCGCAAGTTAGTGTAGATATGCTCTTCAGAAAATATGAAATA	1920
Qy	1921	GGGAGAGACTTAACATCTAGAACATTTAGATATACCGATTTTAGTAACTCTTTTCATTT	1980
Db	1921	GGGAGAGACTTAACATCTAGAACATTTAGATATACCGATTTTAGTAACTCTTTTCATTT	1980
Qy	1981	AGAGCTAATCCAGATATATTTGGGATAGTGAACACCTCTATTGTGTCAGGTTCTATT	2040
Db	1981	AGAGCTAATCCAGATATATTTGGGATAGTGAACACCTCTATTGTGTCAGGTTCTATT	2040
Qy	2041	AGTAGCGTGAATTTAGAAAGACACAAAGCGGTGAATGCGCTTTACTCTTCCCAAT	2100
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Qy	2101	CGAGATCTGATTTAGAAAGACACAAAGCGGTGAATGCGCTTTACTCTTCCCAAT	2160
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Qy	2161	CAAATCGGGTTTAAACACCGATGTGACGATTCATATTTGATCAAGTATCCATTTAGTG	2220
Db	2161	CAAATCGGGTTTAAACACCGATGTGACGATTCATATTTGATCAAGTATCCATTTAGTG	2220
Qy	2221	GATTTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGAGAAATTTGTCGGAAGATCAA	2280
Db	2221	GATTTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGAGAAATTTGTCGGAAGATCAA	2280
Qy	2281	CATGCGAAGCGACTCAGTGATGAGCGGAAATTTACTTCAAGATCCAAATTCAGAGGATC	2340
Db	2281	CATGCGAAGCGACTCAGTGATGAGCGGAAATTTACTTCAAGATCCAAATTCAGAGGATC	2340
Qy	2341	AATAGACAAACAGACCCGTGGCTGGAGAGGAAGTACAGATATTAACATCAAGAGAGAT	2400
Db	2341	AATAGACAAACAGACCCGTGGCTGGAGAGGAAGTACAGATATTAACATCAAGAGAGAT	2400
Qy	2401	GACGTATTCAAAGAGAAATTAACGTCACTACCGGATACCGTTGATGATGCTATCCAAAG	2460
Db	2401	GACGTATTCAAAGAGAAATTAACGTCACTACCGGATACCGTTGATGATGCTATCCAAAG	2460
Qy	2461	TATTTATATCAGAAAATAGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	2520
Db	2461	TATTTATATCAGAAAATAGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	2520
Qy	2521	GGGTATATCGAGATAGTCAAGATTTAGAAATCTATTGATCGCGTATACCCGTTATGAATTAAG	2580
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Qy	2701	TGTTCTGCGAG 2711	

RESULT 4

A00221

LOCUS

DEFINITION Nucleotide sequence 3 from patent number WO8809812.

ACCESSION A00221

VERSION A00221.1

KEYWORDS GI:14454

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .2711

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BASE COUNT 879 a 442 c 557 g 831 t 2 others

ORIGIN

Query Match 99.5%; Score 2696.2; DB 6; Length 2711;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 2701; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Db 121 AATTTGTTAGCTTTTGTATTTTTCATAAGATGTGCATATGTATTAATCGTGGTAA 180

Qy 181 TGAAAACAGTATCAAACTATCAGAACTTTTGGTAGTTTAAATAAAGGAGGTATTTT 240

Db 181 TGAAAACAGTATCAAACTATCAGAACTTTTGGTAGTTTAAATAAAGGAGGTATTTT 240

Qy 241 ATGGAGCAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 300

Db 241 ATGGAGCAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 300

Qy 301 GTACTTTGGATGAGGAGGAGGATCAACTGGTAAATTAATCAATTTCTGTGCA 360

Db 301 GTACTTTGGATGAGGAGGAGGATCAACTGGTAAATTAATCAATTTCTGTGCA 360

Qy 361 CTGTTTCAGTTCTCGGTATCTAACTTTGTACACAGGGGAGGATTTTAGTTGGATTA 420

Db 361 CTGTTTCAGTTCTCGGTATCTAACTTTGTACACAGGGGAGGATTTTAGTTGGATTA 420

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RESULT 5
A10218
LOCUS

A10218

2711 bp

DNA

linear

PAT 27-JAN-1994

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 VERSION A10218.1 GI:490198
 KEYWORDS Bacillus thuringiensis
 SOURCE Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
 ORGANISM Sanchis,V., Lereclus,D., Menou,G., Lecadet,M.M., Martouret,D. and Dedonder,R.
 REFERENCE 1 (bases 1 to 2711)
 AUTHORS Nucleotide sequence coding for polypeptides exhibiting larvicidal activity against lepidoptera
 TITLE Patent: EP 0295156-A 1 14-DEC-1988;
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 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 2701; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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Qy	1388	TACGTGGTGGTGAAGAGTAGAATTTCTACACCTCAAAATAGCTTTACGTATGCGAGAA	1447	Db	2461	ATCAGAAATAGATGAGTTCGAAATTTAAAGCTTTATACCGTTTAAAGAGGTATA	2520
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Qy	1448	GAGTACGCTTATCTTTTAACTGAATACCGCTTACGAGGATATAGTGTGCGACCTCGG	1507	Db	2521	TCGAAGATAGTCAAGACTTGAATCTTATGGCGCTTTTACCGCTTATGAATTAAGAGGTATA	2580
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Qy	1508	AAGGATATAGTCATGCTTTATGTCATGCAACTTTTGTCAAGAGCTGGAACACCTTTT	1567	Db	2581	TAAATGTGCGAGGACACGGGTTCTTATGGCGCTTTTACCGCTTATGAATTAAGAGGTATA	2640
Db	1501	AAGGATATAGTCATGCTTTATGTCATGCAACTTTTGTCAAGAGCTGGAACACCTTTT	1560	Qy	2648	GTGGAGAACCGAATTCGATCGCGGCCACCTTGCATTTGGAATCTGATTTGCTCT	2707
Qy	1568	TACACTGCTGTAGTATTTTCTTGGAGGATCTGAGTCAACTCTTCAAAATACAAATG	1627	Db	2641	GTGGAGAACCGAATTCGATCGCGGCCACCTTGCATTTGGAATCTGATTTGCTCT	2700
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Db	1621	ATCCAGAGAAATTAACAAATACCTTTAGTGAAGGATTTAGTGTGGGGGACCT	1680				
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A31099
LOCUS A31099 3923 bp DNA linear PAT 16-JAN-1996
DEFINITION B.thuringiensis br15 gene from patent EP0408403.
ACCESSION A31099
VERSION A31099.1 GI:1247756
KEYWORDS
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1 (bases 1 to 3923)
AUTHORS Van Mellaert, H., Botterman, J., Van Rie, J., and Joos, H.
TITLE Prevention of Bt resistance development
JOURNAL Patent: EP 0408403-A 3 16-JAN-1991;
PLANT GENETIC SYSTEMS, N.V.
FEATURES
Location/Qualifiers
1..3923
/organism="Bacillus thuringiensis"
/mol_type="genomic DNA"
/db_xref="taxon:1428"
BASE COUNT 1304 a 636 c 849 g 1134 t
ORIGIN

Query Match 98.3%; Score 2664; DB 6; Length 3923;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2679; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 8 AATAGAACTCTCAAACTCTCGATGACTGCTTGTAGTCTTTTAAATATCTGCTACTGCTACCTGACAGGGG 67
DB 1 AATAGAACTCTCAAACTCTCGATGACTGCTTGTAGTCTTTTAAATATCTGCTACTGCTACCTGACAGGGG 60
QY 68 TAGGAACATAATCGGTCAAATTTTAAATATGCGGCATATATGTATATTTTATAAAATTTGT 127
DB 61 TAGGAACATAATCGGTCAAATTTTAAATATGCGGCATATATGTATATTTTATAAAATTTGT 120
QY 128 TAGCTTTTGTATTTTTCATAGATGTGTATATGTATATTAATCGTGTATGAAAAA 187
DB 121 TAGCTTTTGTATTTTTCATAGATGTGTATATGTATATTAATCGTGTATGAAAAA 180
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DB 181 CAGTATCAAACTATCAGAACTTTGGTAGTTTAAATAAAAAAGCGAGGTATTTTATGAGG 240
QY 248 AAAATATCAAAATCAATGATACCTTACAAATTTGTTTAAATAGTAACTCTGAAAGAGTACTTT 307
DB 241 AAAATATCAAAATCAATGATACCTTACAAATTTGTTTAAATAGTAACTCTGAAAGAGTACTTT 300
QY 308 TGGATCGAAGACGGATCAACTGGTAAATCTCAATTTGATATTTCTCTGCTACTGTTTC 367
DB 301 TGGATCGAAGACGGATCAACTGGTAAATCTCAATTTGATATTTCTCTGCTACTGTTTC 360
QY 368 AGTTTCTGGTATCTAACTTTGTACAGGGGGAGATTTTGTAGTTGATTAATAGATTG 427
DB 361 AGTTTCTGGTATCTAACTTTGTACAGGGGGAGATTTTGTAGTTGATTAATAGATTG 420
QY 428 TATGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTTGAACAAATTA 487
DB 421 TATGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTTGAACAAATTA 480
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QY 1448 GAGGTACGTTGATTTCTTAACTGAATTTACGCTGAGGATTAATAGTGTGCCACCTCGCG 1507
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Db	2221	TATCAGATGAATTTTGTCTCGATGAAAGCGGAGTATTCGCGAGAAAGTCAAAACATGCGA	2280
QY	2288	AGCGACTCAGTGATGAGCGGAATTTACTTCAAGATCCAAACTTCAGAGGATCCAAATGAC	2347
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QY	2348	AACCGACCGTGGCTGGAGAGAAATACAGATATTAACATCCAACTTCAGAGGATCCAAATGAC	2407
Db	2341	AACCGACCGTGGCTGGAGAGAAATACAGATATTAACATCCAACTTCAGAGGATCCAAATGAC	2400
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RESULT 9
AR032226
LOCUS
DEFINITION
Sequence 4 from patent US 5866784.
ACCESSION
AR032226
VERSION
AR032226.1
GT:5946515
KEYWORDS

SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 3923)	
TITLE	Van Mellaert,H., Botterman,J., Van Rie,J. and Joos,H.	
JOURNAL	Recombinant plant expressing non-competitively binding insecticidal	
FEATURES	crystal proteins	
source	Patent: US 5866784-A 4 02-FEB-1999;	
BASE COUNT	Location/Qualifiers	
ORIGIN	1. 3923	
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Best Local Similarity	99.1%; Pred. No. 0;	
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QY 1148 TATTGAATATCTTACAACTTTTACGATTTGGTTAGTTGTGGACGCAATTTTATTTGGG 1207
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DB 1321 CTTTATCAATCTCTACTTTACGATTTATACGCAACCTTGCACGCGCCACCACTTTTAAAT 1380
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DB 2701 GCAG 2704

RESULT 10
ARI25059
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

ARI25059
Sequence 7 from patent US 6172281.
ARI25059
ARI25059.1 GI:14110453

Unknown.
Unclassified.
1 (bases 1 to 3923)

Van Mellaert H., Botterman J., Van Rie, J. and Joos, H.
Recombinant plant expressing non-competitively binding BT
insecticidal crystal proteins
Patent: US 6172281-A 7 09-JAN-2001;
Location/Qualifiers

linear PAT 16-MAY-2001

[illegible]

ORGANISM. Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1 (bases 1 to 3646)
AUTHORS Kao S.-S. and Hsieh, F.-C.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-2002) Biopesticide, Taiwan Agricultural Chemical and Toxic Substances Research Institute, COA, 11 Kuang Ming Road, Wu Feng, Taichung Hsien, Taiwan 413, Republic of China
LOCATION/Qualifiers

FEATURES

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BASE COUNT 1202 a 605 c 805 g 1034 t
ORIGIN

Query Match 90.2%; Score 2446.6; DB 1; Length 3646;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2461; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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2401

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2711

Db

2461

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RESULT 13

A43696

LOCUS

DEFINITION

Sequence 1 from Patent WO9506730.

ACCESSION

A43696

VERSION

A43696.1

GI:2298883

KEYWORDS

Bacillus thuringiensis

SOURCE

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

ORGANISM

Bosch, H.J. and Stiekema, W.J.

REFERENCE

1 (bases 1 to 3567)

AUTHORS

HYBRID TOXIN

TITLE

Patent: WO 9506730-A 1 09-MAR-1995;

JOURNAL

SANDOZ LTD (CH)

COMMENT

Other publication BR 9407377 960716

Other publication PL 31317 960624

Other publication CA 2168011 950309

Other publication AU 7693294 950322.

FEATURES

Location/Qualifiers

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ORIGIN

Query Match

89.7%; Score 2431; DB 6; Length 3567;

Best Local Similarity

99.0%; Pred. No. 0;

Matches

2446; Conservative

25; Indels

0; Gaps

0;

Qy

241

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RESULT 14
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ACCESSION AR000001
VERSION AR000001.1 GI:3962532
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3567)
AUTHORS Bosch,H.Jan. and Stiekema,W.Johannes.
TITLE Hybrid toxin.
JOURNAL Patent: US 5736131-A 1 07-APR-1998;
FEATURES
source location/Qualifiers
1..3567 /organism="unknown"
BASE COUNT 1168 a 596 c 792 g 1011 t
ORIGIN

Query Match 89.7%; Score 2431; DB 6; Length 3567;
Best Local Similarity 99.0%; Pred.No. 0;
Matches 2446; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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Search completed: October 13, 2003, 08:17:12
Job time : 12731 secs

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DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
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RC STRAIN=LBIT-147;
RT Barboza-Corona J.E., Lopez-Meza J.E., Ibarra J.E.;
RT "Cloning and expression of the cyt15A4 gene of Bacillus thuringiensis
RT and the comparative toxicity of its gene product.";
RL World J. Microbiol. Biotechnol. 14:437-441(1998).
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DR HSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 13:20:23 ; Search time 25 Seconds
(without alignments)
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Searched: 127863 seqs, 47026705 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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31	1490	34.2	1169	1 C8BA_BACTU	Q45705 bacillus th
32	1403	32.2	1163	1 CQAA_BACTP	Q9X597 bacillus th
33	1396	32.0	1157	1 C8AA_BACTK	Q45704 bacillus th

ALIGNMENTS

RESULT 1

ID	CICA_BACTE	STANDARD;	PRT;	1189 AA.
AC	P05518; P10327; Q03742; Q45725;			
DT	01-NOV-1988 (Rel. 09, Created)			
DT	30-MAY-2000 (Rel. 35, Last sequence update)			
DE	Pesticidal crystal protein cryIa (insecticidal delta-endotoxin)			
DE	CRYIC(a) (CRYIC(a) OR CRYIC)			
GN	CRYIC(a) OR CRYIC(a) OR CRYIC			
OS	Bacillus thuringiensis (subsp. entomocidus), and			
OS	Bacillus thuringiensis (subsp. aizawai).			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1436, 1433;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=B.t. entomocidus; STRAIN=60.5;			
RX	MEDLINE=88289380; PubMed=3399402;			
RA	Honee G., van der Salm T.P.M., Visser B.;			
RT	"Nucleotide sequence of crystal protein gene isolated from B.			
RT	thuringiensis subspecies entomocidus 60.5 coding for a toxin highly			
RT	active against Spodoptera species."			
RL	Nucleic Acids Res. 16:6240-6240(1988).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=B.t. aizawai; STRAIN=NRRL B-19484 / PS811;			
RX	Payne J.M., Sick A.J.;			
RA	"Bacillus thuringiensis isolate active against lepidopteran pests, and			
RT	genes encoding novel lepidopteran-active toxins."			
RL	Patent number US5246852, 21-SEP-1993.			
RN	[3]			
RP	SEQUENCE OF 1-823 FROM N.A.			
RC	SPECIES=B.t. aizawai; STRAIN=7-29;			
RX	MEDLINE=89343627; PubMed=2548060;			
RA	Sanchez V., Lerechus D., Menou M., Chauvaux J., Guo S., Lecadet M.-M.;			
RT	"Nucleotide sequence and analysis of the N-terminal coding region of			
RT	the Spodoptera-active delta-endotoxin gene of Bacillus thuringiensis			
RL	aizawai 7.29."			
RN	[4]			
RP	SEQUENCE OF 1-756 FROM N.A.			
RC	SPECIES=B.t. aizawai; STRAIN=7-29 / K26-21;			
RA	Strizhov N.;			
RL	Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT			
CC	EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE INCLUDING SPODOPTERA			
CC	SPECIES.			
CC	-1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING			
CC	SPOROULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART			
CC	OF THE SPORE COAT.			
CC	-1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE			
CC	N-TERMINUS.			
CC	-1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.			
CC	-----			
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Q45733 bacillus th
Q45709 bacillus th
Q45752 bacillus th
O06014 bacillus th
Q9xdl1 bacillus th
O87404 bacillus th
Q9xnl9 bacillus th
Q45706 bacillus th
Q99031 bacillus th
Q9x682 bacillus th
P17969 bacillus th
P07130 bacillus th

34 1381 31.7 1157 1 C9CA_BACTO
35 1340.5 30.6 719 1 C1IB_BACTE
36 1331.5 30.6 719 1 C1IA_BACTK
37 1328.5 30.5 1169 1 C9DA_BACTP
38 1301.5 29.9 719 1 C1ID_BACTU
39 1246.5 28.6 719 1 C1IC_BACTU
40 1234.5 28.3 1150 1 C9EA_BACTA
41 1125.5 25.8 1160 1 C8CA_BACTP
42 1042.5 23.9 1156 1 C9AA_BACTG
43 947.5 21.7 1109 1 CSAA_BACTF
44 921.5 21.1 659 1 C3BA_BACTO
45 912.5 20.9 644 1 C3AA_BACTT

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CC      EMBL; X07518; CAA30396.1; -
DR      EMBL; M73251; AAA22343.1; -
DR      EMBL; X13620; CAA31951.1; -
DR      EMBL; X96682; CAA65457.1; -
DR      PIR; S00944; S00944
DR      PIR; S04181; S04181
DR      HSP; P02965; 1C1Y
DR      InterPro; IPR001178; Endotoxin
DR      InterPro; IPR005638; endotoxin_C
DR      InterPro; IPR005639; endotoxin_N
DR      Pfam; PF00555; endotoxin; 1
DR      Pfam; PF03944; endotoxin_C; 1
DR      Pfam; PF03945; endotoxin_N; 1
DR      KW Toxin; Sporulation.
FT      CONFLICT 124
FT      CONFLICT 124
FT      CONFLICT 294
FT      CONFLICT 366
FT      CONFLICT 376
FT      CONFLICT 376
FT      CONFLICT 380
FT      CONFLICT 386
FT      CONFLICT 386
FT      CONFLICT 405
FT      CONFLICT 405
FT      CONFLICT 453
FT      CONFLICT 453
FT      CONFLICT 775
FT      CONFLICT 775
FT      CONFLICT 853
FT      CONFLICT 853
FT      CONFLICT 864
FT      CONFLICT 864
FT      CONFLICT 931
FT      CONFLICT 931
FT      SEQUENCE 1189 AA; 134715 MW; 36276B685916A0DF CRC64;

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541	STGVGGQVSNVNPLOKTMETIGENLTSRFRVYDFSNPFSFRANPDIIGISQPLFGAGSI	600
541	STGVGGQVSNVNPLOKTMETIGENLTSRFRVYDFSNPFSFRANPDIIGISQPLFGAGSI	600
601	SSGELYIDKIIILLADATPEASDLERAQKAVNALFTSSNQIGLKTVDYHIDQVSNLV	660
601	SSGELYIDKIIILLADATPEASDLERAQKAVNALFTSSNQIGLKTVDYHIDQVSNLV	660
661	DCLSDFEFLCKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPRDGRWGSTDITIOGGD	720
661	DCLSDFEFLCKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPRDGRWGSTDITIOGGD	720
721	DVFKNYVTLPGTVDECPYLYOKIDSKLKATVRYELRGYIEDSQDLIELVLYANAKH	780
721	DVFKNYVTLPGTVDECPYLYOKIDSKLKATVRYELRGYIEDSQDLIELVLYANAKH	780
781	EIVNVPGTGSLWPLSAQSPGKCGENPCAPHELWNPDLDCSC	823
781	EIVNVPGTGSLWPLSAQSPGKCGENPCAPHELWNPDLDCSC	823

RESULT 2

ID	C1CB_BACTG	STANDARD;	PRT;	1176 AA.
AC	P56953;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Pesticidal crystal protein cryIcB (insecticidal delta-endotoxin			
DE	CryIC(b)) (crystalline entomocidal protoxin) (133 kDa crystal protein).			
GN	CryICB OR CryIC(B).			
OS	Bacillus thuringiensis (subsp. galleriae).			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_Taxid:29338;			
RP	SEQUENCE FROM N.A.			
RP	[1]			
RC	STRAIN=HD-29;			
RC	MEDLINE=93236401; PubMed=8476286;			
RA	Kalman S.S.;			
RA	"Cloning a novel cryIC-type gene from a strain of Bacillus			
RL	thuringiensis galleriae."			
RL	Appl. Environ. Microbiol. 59:1131-1137(1993).			
CC	-1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT			
CC	EPITHELIAL CELLS OF INSECTS. TOXIC TO SPODOPTERA EXIGUA AND			
CC	TRICHLUPSTIA NI.			
CC	-1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING			
CC	SPOREATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART			
CC	OF THE SPORE COAT.			
CC	-1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE			
CC	N-TERMINUS.			
CC	-1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.			
CC	-----			
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; M97880; -; NOT ANNOTATED_CDS.			
DR	PIR; A48970; A48970.			
DR	HSSP; P02965; LC1Y.			
DR	InterPro; IPR001178; Endotoxin.			
DR	InterPro; IPR005638; endotoxin_C.			
DR	InterPro; IPR005639; endotoxin_N.			
DR	Pfam; PF00555; endotoxin; 1.			
DR	Pfam; PF03944; endotoxin_C; 1.			
DR	Pfam; PF03945; endotoxin_N; 1.			
DR	Toxin; Sporulation.			
SK	SEQUENCE 1176 AA; 132867 MW; 108233494C2AC018 CRC64;			

Query Match 80.2%; Score 3495.5; DB 1; Length 1176;



Best Local Similarity 80.7%; Pred. No. 7.1e-240;
Matches 668; Conservative 48; Mismatches 89; Indels 23; Gaps 4;

QY 1 MEENNOQCPYNCLSNPEVLDDGERISTGSSIDISLVQFLVSNVPGGFLVGLI 60
DB 1 MENNIOQCPYNCLSNPEVLDDGERISTGSSIDISLVQFLVSNVPGGFLVGLI 60

QY 61 DFMVGVPSQWDAFVQIQLINERIAEPARNAATANLEGNNFNIVYAEKWEEDP 120
DB 61 DFMVGVPSQWDAFVQIQLINERIAEPARNAATANLEGNNFNIVYAEKWEEDP 120

QY 121 NNPATRVIDRFRILDLGLERDIPSRISGSEVPPLLSVYQAANLHAILRDSVIFGR 180
DB 121 DNPVTRVDRFRILDLGLERDIPSRISGSEVPPLLSVYQAANLHAILRDSVIFGR 180

QY 181 WGLTINNVNENYRLIRHIDEVADHCANTYNGLNLPKSTYQDMWITYNRLRDLTLVL 240
DB 181 WGLTINNVNENYRLIRHIDEVADHCANTYNGLNLPKSTYQDMWITYNRLRDLTLVL 240

QY 241 DIAAFPNDYRRYPIQVQQLTREVYDPLINFPQLQSVLAQLPTFNVMSSAIRNPHL 300
DB 241 DIAAFPNDYRRYPIQVQQLTREVYDPLINFPQLQSVLAQLPTFNVMSSAIRNPHL 300

QY 301 FDLANLTIPTDFWFSVGRNPFYWGCHRVISLGGNITSPYIGREANQPPRSFTFNGPV 360
DB 301 FDLANLTIPTDFWFSVGRNPFYWGCHRVISLGGNITSPYIGREANQPPRSFTFNGPV 360

QY 361 FRTLSTPTLRLQPCORHFNLRGGEVGFSTPTNSFTYRGRTVDSLTLPPEEDNSVP 420
DB 361 FRTLSTPTLRLQPCORHFNLRGGEVGFSTPTNSFTYRGRTVDSLTLPPEEDNSVP 420

QY 421 PREGYSHRLCHATFVQSGTPELTGVPFVSWTHRSATLNTIDPERINQIPLVKGFRVMG 480
DB 421 PREGYSHRLCHATFVQSGTPELTGVPFVSWTHRSATLNTIDPERINQIPLVKGFRVMG 480

QY 481 GTSVITGPGTGDILRRFTGDFVSLQVNSPITQRLRFRVASSRDARVIVLTGAA 540
DB 481 GTSVITGPGTGDILRRFTGDFVSLQVNSPITQRLRFRVASSRDARVIVLTGAA 540

QY 541 STGVGGQVSNVPLQKTMIGENLSTRPTRYTDFGNPPFRANPDIGISEQLPGAG-S 599
DB 541 STGVGGQVSNVPLQKTMIGENLSTRPTRYTDFGNPPFRANPDIGISEQLPGAG-S 599

QY 599 SVTVGGSTTNGOGFFSTMSANGALTSQSFRFAEP-----VGLSAGSQGASIS 582
DB 599 SVTVGGSTTNGOGFFSTMSANGALTSQSFRFAEP-----VGLSAGSQGASIS 582

QY 600 ISSG-----ELYIKIEIILADATPEASDLERAQKAVNALFTSSNQIGLKTVDYHDQ 655
DB 600 ISSG-----ELYIKIEIILADATPEASDLERAQKAVNALFTSSNQIGLKTVDYHDQ 655

QY 655 VSNLVDCLSDFCDEKRELSKVKHAKLSDERNLLQDPNFRGNGRQDGRWGSTDIT 715
DB 655 VSNLVDCLSDFCDEKRELSKVKHAKLSDERNLLQDPNFRGNGRQDGRWGSTDIT 715

QY 715 IOGGDDVRKENYVTLPGTVDECVPTLYOKIDESKIKAYTRYELRGYIEDSDLEIYLIA 775
DB 715 IOGGDDVRKENYVTLPGTVDECVPTLYOKIDESKIKAYTRYELRGYIEDSDLEIYLIA 775

QY 775 YNAKHEIVNVPGTGSIMPLSAQSPICKGCEPNRCAPHLEWNPDLDCSC 823
DB 775 YNAKHEIVNVPGTGSIMPLSAQSPICKGCEPNRCAPHLEWNPDLDCSC 823

QY 823 YNAKHEIVNVPGTGSIMPLSAQSPICKGCEPNRCAPHLEWNPDLDCSC 810
DB 823 YNAKHEIVNVPGTGSIMPLSAQSPICKGCEPNRCAPHLEWNPDLDCSC 810

RESULT 3
ID C1EA BACTX STANDARD; PRT; 1171 AA.
AC Q57458; Q03741;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cryIEa (insecticidal delta-endotoxin
DE CryIE(a) (crystalline entomocidal protoxin) (133 kDa crystal protein).
GN CRYIEA OR CRYIE(A) OR CRYIC(B) OR BTXI OR BTL1.
OS Bacillus thuringiensis (subsp. kenya).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=33930;

SEQUENCE FROM N.A.
MEDLINE=91081338; PubMed=2259636;
Boese M., Masson L., Brousseau R.;
"Nucleotide sequence of a novel crystal protein gene isolated from
Bacillus thuringiensis subsp. kenya";
Nucleic Acids Res. 18:7443-7443(1990).
SEQUENCE FROM N.A.
STRAIN=4F1;
MEDLINE=91072224; PubMed=2254254;
Visser B., Munsterman E., Stoker A., Dirkse W.G.;
"A novel Bacillus thuringiensis gene encoding a Spodoptera exigua-
specific crystal protein";
J. Bacteriol. 172:6783-6788(1990).
SEQUENCE FROM N.A.
STRAIN=PS81F;
Payne J.M., Sick A.J.;
"Novel Bacillus thuringiensis isolate denoted B.t. PS81F, active
against lepidopteran pests, and a gene encoding a lepidopteran-active
toxin";
Patent number US039523, 13-AUG-1991.
-!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE INCLUDING SPODOPTERA
SPECIES.
-!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
OF THE SPORE COAT.
-!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
N-TERMINUS.
-!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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EMBL; X56144; CAA39609.1; -;
EMBL; X53985; CAA37933.1; -;
EMBL; M73252; AAA22345.1; -;
PIR; I40572; I40572.
HSP; P02965; 1CIY.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin C.
InterPro; IPR005639; endotoxin N.
Pfam; PF00555; endotoxin_1.
Pfam; PF03944; endotoxin_1.
Pfam; PF03945; endotoxin_N; 1.
Toxin; Sporulation.
FT CONFLICT 862 862 N -> K (IN REF. 3).
SQ SEQUENCE 1171 AA; 133252 MW; 5758FBESABDSABE CRC64;
Query Match 61.5%; Score 2680; DB 1; Length 1171;
Best Local Similarity 64.5%; Pred. No. 5.3e-182;
Matches 536; Conservative 88; Mismatches 169; Indels 38; Gaps 15;

QY 4 NNQNCIPYCNCLSNPEVLDDGERISTGSSIDISLVQFLVSNVPGGFLVGLIDF 62
DB 4 NNQNCIPYCNCLSNPEVLDDGERISTGSSIDISLVQFLVSNVPGGFLVGLIDF 62

QY 5 NNQNCIPYCNCLSNPEVLDDGERISTGSSIDISLVQFLVSNVPGGFLVGLIDF 61
DB 5 NNQNCIPYCNCLSNPEVLDDGERISTGSSIDISLVQFLVSNVPGGFLVGLIDF 61

QY 63 WGVIGVPSQWDAFVQIQLINERIAEPARNAATANLEGNNFNIVYAEKWEEDPN 122
DB 63 WGVIGVPSQWDAFVQIQLINERIAEPARNAATANLEGNNFNIVYAEKWEEDPN 122

QY 62 IWGIGVPSQWDAFVQIQLINERIAEPARNAATANLEGNNFNIVYAEKWEEDPN 121
DB 62 IWGIGVPSQWDAFVQIQLINERIAEPARNAATANLEGNNFNIVYAEKWEEDPN 121

QY 123 PATRVIDRFRILDLGLERDIPSRISGSEVPPLLSVYQAANLHAILRDSVIFGR 182
DB 123 PATRVIDRFRILDLGLERDIPSRISGSEVPPLLSVYQAANLHAILRDSVIFGR 182

QY 122 PALKEEMTQNDMNSILVTAIPULFSVQNYQVPLSVYQAANLHLSVLRDSVIFGR 181
DB 122 PALKEEMTQNDMNSILVTAIPULFSVQNYQVPLSVYQAANLHLSVLRDSVIFGR 181

QY 183 LTTINNVNENYRLIRHIDEVADHCANTYNGLNLPKSTYQDMWITYNRLRDLTLVL 241
DB 183 LTTINNVNENYRLIRHIDEVADHCANTYNGLNLPKSTYQDMWITYNRLRDLTLVL 241

Db 182 FDIATNSRYNDLTRLIPIYDYAVRWYNTGLDRFLPGRGLRNWARFNQFRRLTISVLD 241
 Qy 242 IAAFFPNYONRYPQVPQVGLTREVYDPLINPFLQVQAQPTFNVMESAINRPHLF 301
 Db 242 IISFRNYSRLYPPTSSQLTREVYDVPVINTYRVG-----PSFENIENSAIRSPHLM 297
 Qy 302 DILNNLTFTDWFSGVRNFGWGHVRVSSLIIGGN-ITSPYIGREANQPPRSF---TFN 357
 Db 298 DFLNNLTFTD--LIRGVHYWAGHRVTSHTSGSSQVITTPQYGITANASPRRTIAPSTFP 355
 Qy 358 G--PVFETLSIPTLRLLQPCORHNNLGRGGVFSFPTNS-PTVRGRTGVDSTLELPP 414
 Db 356 GLNLFYKTLNPFRRSENITPTLGINV--VQGVFIQPNNAEVLVRSRTGVDLSNELPI 413
 Qy 415 E-DNSVPPREGVSHRLCHATFVQSGTPELTTCGVVFSWTHRSATLNTIDPERINOIPLV 473
 Db 414 DGENSL---VGVSHRLSHVTLTRSLYNTNLSLPTFVWHHSATNTINPDIIITQIDPLV 470
 Qy 474 KGRVWGGTSVITGPGFTGGDILRRNTFGDFVSLQVNSPITQRYLRFVASSRDARV 533
 Db 471 KGRVWGGTSVITGPGFTGGDILRRNTFGDFVSLQVNSPITQRYLRFVASSRDARV 530
 Qy 534 IYLVGAASGCGVQVSNMPLQKTMETIGENLTSRFRVYDFSNPFSFRANPDIIIGISEQ- 592
 Db 531 TV-----AIGQIRVDMTLEKTMETIGESLTSRFSYTNFNSPFSFRANPDIIIRAEEL 583
 Qy 593 PLFAGSISSEGLYIDKIEIILADATFEASDLERAQKAVNALFTSNQIGLKTVDYD 652
 Db 584 PIRG-----GELYIDKIEIILADATFEEDYDLERAQKAVNALFTSNQIGLKTVDYD 637
 Qy 653 IDQVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGNRQPDGRWGST 712
 Db 638 IDQVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGNRQPDGRWGST 697
 Qy 713 DITIQGDDVFNKENVYTLPGTVDCYPTLYOKIDESKLYATRYELRGVIEDSDLEIY 772
 Db 698 DITIQGDDVFNKENVYTLPGTVDCYPTLYOKIDESKLYATRYELRGVIEDSDLEIY 757
 Qy 773 LIYANAKHETVNVPGTGLMPLSAQSPIGKCGPNRCAPHLEWNPDLDCSC 823
 Db 758 LIRYANAKHETVNVPGTGLMPLSAQSPIGKCGPNRCAPHLEWNPDLDCSC 808

RESULT 4
 ID CLDB_BACTU STANDARD; PRT; 1160 AA.
 AC Q45747;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Pesticidal crystal protein cryIb (insecticidal delta-endotoxin
 DE CryID(b)) (Crystalline entomocidal protoxin) (131 kDa crystal protein).
 GN CRYIDB OR CRYID(B).
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BTS0349A;
 RA Lambert B.;
 RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF INSECTS.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPORE FORMATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; Z22511; CAA80234.1; -
 DR PIR; S32647; S32647.
 DR HSSP; P02965; 1CIY.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR Pfam; PF00555; endotoxin_1.
 DR Pfam; PF03944; endotoxin_C.
 DR Pfam; PF03945; endotoxin_N.
 KW Toxin; Sporulation.
 SQ SEQUENCE 1160 AA; 130968 MW; B18B18748B40695E CRC64;
 Query Match 59.3%; Score 2584; DB 1; Length 1160;
 Best Local Similarity 61.9%; Pred No 3 4e-175;
 Matches 513; Conservative 80; Mismatches 200; Indels 36; Gaps 12;
 Qy 1 MEENQNCIPYCNLSNDEEVLDGERISTGNSSIDISLVQFLVSNFVGGGLVGLI 60
 Db 1 MDINHQCIPYCNLSNDEEVLDGERISTGNSSIDISLVQFLVSNFVGGGLVGLI 60
 Qy 61 DFVWGVGSQWDAFLVQIEQLINERIAEPARNAIANLEGLGNFNIVYEAKEWEDP 120
 Db 61 ELIWFVGSQWDAFLVQIEQLINERIAEPARNAIANLEGLGNFNIVYEAKEWEDP 120
 Qy 121 NNPATRVTRIDFRILDGLERIDPSRISGFEVPLSVYAAQANLHAILRDSVIFGER 180
 Db 121 SNPALREEMRTQFNVMNSALIAAIPLLRVNTEVALLSVYVQAANLHSLVDRVSYQOR 180
 Qy 181 WGLTNTNVNENLRIRHIDYADHCANTYNGRLNLPKSTYQDWITYNLRDLTLTVL 240
 Db 181 WGFDPATVNSRYSDLTRLHVYTTDCHCVTDYNDGLNLEGRSLSDVWVYVNRFRRLTISVL 240
 Qy 241 DIAAFPNDNRYPQVQGLTREVYD--PLINFPOLQVQAQPTFNVMESAINRPH 299
 Db 241 DIAAFPNDNRYPQVQGLTREVYD--PLINFPOLQVQAQPTFNVMESAINRPH 299
 Qy 300 LFDILNNLTFTDWFSGVRNFGWGHVRVSSLIIGGN-ITSPYIGREANQPPRSF 357
 Db 299 LVDFLNSFTIYD--SLASYAYWGGHVLNSFRITGTTNLRSLYRGEGNTERPVTISAS 356
 Qy 358 G--PVFETLSIPTLRLLQPCORHNNLGRGGVFSFPTNSFTYRGRGTVDSLTELPE 415
 Db 357 PSVPIFETLSYFTGLNNPN-----VAGIEGVFQNTISRSYRKSGLDFSELPPQ 409
 Qy 416 DNSVPPREGVSHRLCHATFVQSGTPELTTCGVVFSWTHRSATLNTIDPERINOIPLV 475
 Db 410 DVSVPALGVSHRLCHATFVQSGTPELTTCGVVFSWTHRSATLNTIDPERINOIPLV 468
 Qy 476 FRVWGGTSVITGPGFTGGDILRRNTFGDFVSLQVNSPITQRYLRFVASSRDARV 535
 Db 469 HTLASGASVTKGFTGGDILRRNTFGDFVSLQVNSPITQRYLRFVASSRDARV 521
 Qy 536 LTGAASGCGVQVSNMPLQKTMETIGENLTSRFRVYDFSNPFSF-RANPDIIIGSEQL 594
 Db 522 ANRSGTFRYSQPPSYGVSFPTKMDAGALTSRFAHTLFTPTFSRAQ-----EEDPL 575
 Qy 595 FGAGSISSEGLYIDKIEIILADATFEASDLERAQKAVNALFTSNQIGLKTVDYD 654
 Db 576 Y-----IQSG-VYDRIEIPVDATFESEINLERAQKAVNALFTSNQIGLKTVDYD 630
 Qy 655 QVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGNRQPDGRWGST 714
 Db 631 QVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGNRQPDGRWGST 690
 Qy 715 TIQGGDDVFNKENVYTLPGTVDCYPTLYOKIDESKLYATRYELRGVIEDSDLEIY 774
 Db 691 TIQGGDDVFNKENVYTLPGTVDCYPTLYOKIDESKLYATRYELRGVIEDSDLEIY 750

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OM protein - protein search, using sw model

Run on: October 9, 2003, 13:20:48 ; Search time 45 Seconds
(without alignments)
1758.818 Million cell updates/sec

Title: US-09-918-485-2
Perfect score: 4358
Sequence: 1 MEENNQOCIPYNCLSNPDE.....GEPNRCAPHLNPNLDSC 823

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4358	100.0	823	S04181	parasporal crystal
2	4275	98.1	1189	S00944	parasporal crystal
3	3495.5	80.2	1176	A48970	parasporal crystal
4	3374	77.4	655	JC7140	protoxin - Bacillus
5	2680	61.5	1171	A37829	parasporal crystal
6	2680	61.5	1171	I40572	parasporal crystal
7	2584	59.3	1160	S32647	parasporal crystal
8	2573	59.0	1165	S11446	parasporal crystal
9	2531.5	58.1	1176	JT0241	parasporal crystal
10	2530.5	58.1	934	A22798	parasporal crystal
11	2525.5	58.0	1176	JC2219	parasporal crystal
12	2518.5	57.8	1176	A22617	parasporal crystal
13	2518.5	57.8	1176	S02215	parasporal crystal
14	2496.5	57.3	1181	A41052	parasporal crystal
15	2378.5	54.6	1155	A26513	parasporal crystal
16	2374.5	54.5	1155	JD0002	parasporal crystal
17	2374.5	54.5	1156	A29125	parasporal crystal
18	2367.5	54.3	1174	A42459	parasporal crystal
19	2363.5	54.2	1155	S02134	parasporal crystal
20	2363.5	54.2	1155	I39838	parasporal crystal
21	2355	54.0	1174	S32649	parasporal crystal
22	2334.5	53.6	1178	USRSXH	parasporal crystal
23	2232	53.5	1177	A49785	parasporal crystal
24	2287.5	52.5	1166	S32645	parasporal crystal
25	2247	51.6	1156	A29838	parasporal crystal
26	2221	51.0	1172	S32689	parasporal crystal
27	1980	45.4	1228	S00873	parasporal crystal
28	1609	36.9	1138	A48944	parasporal crystal
29	1381	31.7	1157	S49247	parasporal crystal

30	1354	31.1	618	2	S11445	parasporal crystal
31	1340.5	30.8	719	2	I40590	crv465 protein -
32	1331.5	30.6	719	2	I39815	insecticidal prote
33	1326	30.4	1154	2	S39536	parasporal crystal
34	1322.5	30.3	719	2	S25383	parasporal crystal
35	1316.5	30.2	719	2	I39814	insecticidal prote
36	1125.5	25.8	1160	2	I40589	parasporal crystal
37	1042.5	23.9	1156	2	S19306	parasporal crystal
38	921.5	21.1	659	2	S10228	parasporal crystal
39	912.5	20.9	652	2	A27323	parasporal crystal
40	907.5	20.8	652	2	I39811	parasporal crystal
41	899	20.6	1136	1	USBS81	parasporal crystal
42	847.5	19.4	934	2	B29838	parasporal crystal
43	839	19.3	1180	2	A26858	parasporal crystal
44	838	19.2	1180	2	I39870	parasporal crystal
45	811.5	18.6	649	1	JH0261	parasporal crystal

ALIGNMENTS

RESULT 1

S04181
parasporal crystal protein - Bacillus thuringiensis (strain aizawai 7.29) (fragment)
N/Alternate names: delta-endotoxin
C/Species: Bacillus thuringiensis
C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-Aug-1999
C/Accession: S04181
R/Sanchis, V.; Lereclus, D.; Menou, G.; Chaufaux, J.; Guo, S.; Lecadet, M.M.
Mol. Microbiol. 3, 229-238, 1989
A/Title: Nucleotide sequence and analysis of the N-terminal coding region of the Spodoptera frugiperda delta-endotoxin
A/Reference number: S04181; MUID:89343627; PMID:2548060
A/Accession: S04181
A/Molecule type: DNA
A/Residues: 1-823 <S>
A/Cross-references: EMBL:X13620; NID:g40355; PIDN:CAA31951.1; PID:g40356
C/Genetics:
A/Gene: bta
C/Superfamily: parasporal crystal protein
C/Keywords: delta-endotoxin

Query Match 100.0%; Score 4358; DB 2; Length 823;
Best Local Similarity 100.0%; Pred. No. 3.3e-307;
Matches 823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEENNQOCIPYNCLSNPDEVLDDGERISTGNSSTDISLSLVQFLVSNFVPGGFLVGLI	60
DB	1	MEENNQOCIPYNCLSNPDEVLDDGERISTGNSSTDISLSLVQFLVSNFVPGGFLVGLI	60
QY	61	DFVMGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGIGNNFNIYVEAFKEWEDP	120
DB	61	DFVMGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGIGNNFNIYVEAFKEWEDP	120
QY	121	NNPATRTRVIDRFRILDLGRLDIPSPRISGFVPLLSVYAQAANLHAILRDSVIGER	180
DB	121	NNPATRTRVIDRFRILDLGRLDIPSPRISGFVPLLSVYAQAANLHAILRDSVIGER	180
QY	181	WGLTTINVENNYNRLIRHIDYADHCANTYNGLNLPKSTVQDWITYNRLRDLTLVL	240
DB	181	WGLTTINVENNYNRLIRHIDYADHCANTYNGLNLPKSTVQDWITYNRLRDLTLVL	240
QY	241	DIAAFFNYDNRYPYIQVGQLTREYVTDPLINFPQLQSVQALPTFNVMESSAIRNPHL	300
DB	241	DIAAFFNYDNRYPYIQVGQLTREYVTDPLINFPQLQSVQALPTFNVMESSAIRNPHL	300
QY	301	FDILNNLTFTDWFSGVGRNFWGGRHVRVSSLIIGGNITSPYIGREANQEPFRSFTNGPV	360
DB	301	FDILNNLTFTDWFSGVGRNFWGGRHVRVSSLIIGGNITSPYIGREANQEPFRSFTNGPV	360
QY	361	FRTLSIPTRLRLQQPCQRHHNLAGGEGVEESTPTNSFTYGRGTVDSLTLPEDNSVP	420
DB	361	FRTLSIPTRLRLQQPCQRHHNLAGGEGVEESTPTNSFTYGRGTVDSLTLPEDNSVP	420

301 FDLNLLNLTFTDMFVSGRNFYWGGRHVSVSSLIQGGNITSPIYGRANQEPSPRFTFNGPV 360
361 FRTLSIPTLRLLQOPQORHFNLRGEGVEFSTPTNSFTYRGRGTVDLSLTLPEDNSVP 420
361 FRTLSNPTLRLLQOPWAPFPFNLRCGVEGFSTPTNSFTYRGRGTVDLSLTLPEDNSVP 420
421 PREGYSHRLCHATFVQSGTTPFLTGGVVFVSWTHRSATLTNTIDPERINQIPLVKGFVWG 480
421 PREGYSHRLCHATFVQSGTTPFLTGGVVFVSWTHRSATLTNTIDPERINQIPLVKGFVWG 480
481 GTSVITGPGFTGCDILRRNTFGDFVSLQVNSINSPITQRYLRFRYASSRDARVILTGAA 540
481 GTSVITGPGFTGCDILRRNTFGDFVSLQVNSINSPITQRYLRFRYASSRDARVILTGAA 540
541 STGVGGQVSNMPLQKTMETGENLTSRTFRYDFSNPFPFRANPDIIGISQPLFGAGSI 600
541 STGVGGQVSNMPLQKTMETGENLTSRTFRYDFSNPFPFRANPDIIGISQPLFGAGSI 600
601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNOIGLKTDTVDYHIDQVSNLV 660
601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNOIGLKTDTVDYHIDQVSNLV 660
661 DCLSDPECLDEKRELSEKVKHAKLSDERNLLQDPNFRGINRQPDGRGWSGTDTITIOGGD 720
661 DCLSDPECLDEKRELSEKVKHAKLSDERNLLQDPNFRGINRQPDGRGWSGTDTITIOGGD 720
721 DVFKNYVTLPGTVDECPYLYQKIDSKLKAYTRYELRGYIEDSDLEIYLIAYNAXH 780
721 DVFKNYVTLPGTVDECPYLYQKIDSKLKAYTRYELRGYIEDSDLEIYLIAYNAXH 780
781 EIVNVPGTSLMPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
781 EIVNVPGTSLMPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 3
A48970
Parasporal crystal protein crylCb - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
C:Accession: A48970
R:Kelman, S.; Kiehne, K.L.; Libs, J.L.; Yanamoto, T.
A:Title: Cloning of a novel cryIC-type gene from a strain of Bacillus thuringiensis subsp.
A:Reference number: A48970; MUID:93236401; PMID:8476286
A:Accession: A48970
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-1176 <KAL>
A:Cross-references: GB:M97880; NID:9289263
A:Experimental source: subsp. galleriae HD29
A:Note: sequence extracted from NCBI backbone (NCBIN:129672, NCBIP:129675)
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 80.2%; Score 3495.5; DB 2; Length 1176;
Best Local Similarity 80.7%; Pred. No. 1.8e-244;
Matches 668; Conservative 48; Mismatches 89; Indels 23; Gaps 4;

QY 1 MEENNONCIPYCNLSNPEEVLIDGERISTGNSSIDISLSVQLVSNFVPGGFLVGLI 60
DB 1 MENNINQCVYCNLSNPEEVLIDGERISTGNSSIDISLSVQLVSNFVPGGFLVGLI 60
QY 61 DFWMGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKEWEDP 120
DB 61 DFWMGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKEWEDP 120
QY 121 NNPATRTRVIDRFRILDGLLERDIPSFRIISGFVEPLLSVYAAANLHLAILRDSVIFGER 180
DB 121 NNPATRTRVIDRFRILDGLLERDIPSFRIISGFVEPLLSVYAAANLHLAILRDSVIFGER 180
QY 181 WGLTINNVNENYRLIRHIDEYADHCANTYNGRLNLPKSTYQDMITTYNRLRDLTLTVL 240
DB 181 WGLTINNVNENYRLIRHIDEYADHCANTYNGRLNLPKSTYQDMITTYNRLRDLTLTVL 240

421 PREGYSHRLCHATFVQSGTTPFLTGGVVFVSWTHRSATLTNTIDPERINQIPLVKGFVWG 480
421 PREGYSHRLCHATFVQSGTTPFLTGGVVFVSWTHRSATLTNTIDPERINQIPLVKGFVWG 480
481 GTSVITGPGFTGCDILRRNTFGDFVSLQVNSINSPITQRYLRFRYASSRDARVILTGAA 540
481 GTSVITGPGFTGCDILRRNTFGDFVSLQVNSINSPITQRYLRFRYASSRDARVILTGAA 540
541 STGVGGQVSNMPLQKTMETGENLTSRTFRYDFSNPFPFRANPDIIGISQPLFGAGSI 600
541 STGVGGQVSNMPLQKTMETGENLTSRTFRYDFSNPFPFRANPDIIGISQPLFGAGSI 600
601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNOIGLKTDTVDYHIDQVSNLV 660
601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNOIGLKTDTVDYHIDQVSNLV 660
661 DCLSDPECLDEKRELSEKVKHAKLSDERNLLQDPNFRGINRQPDGRGWSGTDTITIOGGD 720
661 DCLSDPECLDEKRELSEKVKHAKLSDERNLLQDPNFRGINRQPDGRGWSGTDTITIOGGD 720
721 DVFKNYVTLPGTVDECPYLYQKIDSKLKAYTRYELRGYIEDSDLEIYLIAYNAXH 780
721 DVFKNYVTLPGTVDECPYLYQKIDSKLKAYTRYELRGYIEDSDLEIYLIAYNAXH 780
781 EIVNVPGTSLMPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
781 EIVNVPGTSLMPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 2
S00944
Parasporal crystal protein crylCa1 - Bacillus thuringiensis (strain entomocidus 60.5)
C:Species: Bacillus thuringiensis
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 01-Dec-2000
C:Accession: S00944
R:Honee, G.; van der Salm, T.; Visser, B.
Nucleic Acids Res. 16, 6240, 1988
A:Title: Nucleotide sequence of crystal protein gene isolated from B. thuringiensis subsp.
A:Reference number: S00944; MUID:88289380; PMID:3399402
A:Accession: S00944
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-1189 <HON>
A:Cross-references: EMBL:X07518; NID:940293; PIDN:CAA30396.1; PID:940294
A:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 98.1%; Score 4275; DB 2; Length 1189;
Best Local Similarity 98.7%; Pred. No. 6.2e-301;
Matches 812; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 MEENNONCIPYCNLSNPEEVLIDGERISTGNSSIDISLSVQLVSNFVPGGFLVGLI 60
DB 1 MEENNONCIPYCNLSNPEEVLIDGERISTGNSSIDISLSVQLVSNFVPGGFLVGLI 60
QY 61 DFWMGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKEWEDP 120
DB 61 DFWMGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKEWEDP 120
QY 121 NNPATRTRVIDRFRILDGLLERDIPSFRIISGFVEPLLSVYAAANLHLAILRDSVIFGER 180
DB 121 NNPATRTRVIDRFRILDGLLERDIPSFRIISGFVEPLLSVYAAANLHLAILRDSVIFGER 180
QY 181 WGLTINNVNENYRLIRHIDEYADHCANTYNGRLNLPKSTYQDMITTYNRLRDLTLTVL 240
DB 181 WGLTINNVNENYRLIRHIDEYADHCANTYNGRLNLPKSTYQDMITTYNRLRDLTLTVL 240
QY 241 DIAAPFNVDNRRYPIQVQGLTRVYTDPLNFNPNQVLAQLPFNFMWESSAIRNPHL 300
DB 241 DIAAPFNVDNRRYPIQVQGLTRVYTDPLNFNPNQVLAQLPFNFMWESSAIRNPHL 300
QY 301 FDLNLLNLTFTDMFVSGRNFYWGGRHVSVSSLIQGGNITSPIYGRANQEPSPRFTFNGPV 360
DB 301 FDLNLLNLTFTDMFVSGRNFYWGGRHVSVSSLIQGGNITSPIYGRANQEPSPRFTFNGPV 360

Db 181 WGLTTINVENYNNRLIRHIDEYANHCADTYNRLGNLPLKSTYQDMWITYNRLRDLTLTVL 240
QY 241 DIAAFPPNNDNRYPYQPVGQLTRVYTDPLINFPQLQSVLAQLPTFNWESSAIRNPHL 300
Db 241 DIAAFPPNNDNRYPYQPVGQLTRVYTDPLINFPQLQSVLAQLPTFNWESSAIRNPHL 300
QY 301 FDLNNLTITFTDFSGVGRFPGCHRVISLIGCGNITSPIYGRANQBPSPFTFNGPV 360
Db 301 FDLNNLTITFTDFSGVGRFPGCHRVISLIGCGNITSPIYGRANQBPSPFTFNGPV 360
QY 361 FRTLSPITLRLLOQPCORHFNLRGEGVEFSTPTNSFTYRGRTVDSLTLPEDNSVP 420
Db 361 FRTLSPITLRLLOQPCORHFNLRGEGVEFSTPTNSFTYRGRTVDSLTLPEDNSVP 420
QY 421 PREGYSHRLCHATFVQSGTPTLTTGVVFSWTHRSATLNTIDPERINOIPLVKGRVWG 480
Db 421 PREGYSHRLCHATFVQSGTPTLTTGVVFSWTHRSATLNTIDPERINOIPLVKAFNLTS 480
QY 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNSPITQRYLRFYASSRDARVILVTGAA 540
Db 481 GTSVVRGPGTGGDILRRNTFGDFVSLQVNSPITQRYLRFYASSRDARVILVTGAA 540
QY 541 STVGGOVSVNMPLOKTMIEGNLTSRTFRYTDPSNPPSFRANPDIIIGISEQPLFCAG-S 599
Db 534 SVTVGGSTTGQGFSTMSANGALTSQSFRFAEP-----VGISAGSQGASIS 582
QY 600 ISSG-----ELYDKIEIILADATFEAESDLERAQKAVNALFTSSNOIGLKTVDYHIDQ 655
Db 583 ISNVGRQMFHLDRIEFLVPTSTFEEDYDLERAQKAVNALFTSTNQLGLKTVDYHIDQ 642
QY 656 VSNLVDCLSEDFCLDEKRLSEKVKHAKLSBERNLLQPNFRGINQPDRCWRGSTDIT 715
Db 643 VSNLVECLSEDFCLDEKRLSEKVKHAKLSBERNLLQPNFRSINGQLDRCWRGSTDIT 702
QY 716 IOGGDDVFNENYVTLPGTVDCEVPTLYOKIDESKLKATRYELRGYIEDSODLEYLIA 775
Db 703 IOGGDDVFNENYVTLPGTVDCEVPTLYOKIDESKLKATRYELRGYIEDSODLEYLIR 762
QY 776 YNAKHEIVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
Db 763 YNAKHEIVNVPGTSLWPLSIENSIGPCGEPNRCAPHLEWNPDLDCSC 810

RESULT 4
JC7140
prototoxin - Bacillus thuringiensis
N.Alternate names: cryIC protein
C.Species: Bacillus thuringiensis
C.Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
C.Accession: JC7140
R.Christov, N.K.; Imaishi, H.; Ohkawa, H.
Biosci. Biotechnol. Biochem. 63, 1433-1444, 1999
A.Title: Green-tissue-specific expression of a reconstructed cryIC gene encoding the act
protera litura.
A.Reference number: JC7140; MUID:99430790; PMID:10501003
A.Accession: JC7140
A.Molecule type: DNA
A.Residues: 1-655 <CHR>
A.Cross-references: EMBL:X96682
C.Genetics:
A.Gene: cryIC
C.Superfamily: parasporal crystal protein

Query Match 77.4%; Score 3374; DB 2; Length 655;
Best Local Similarity 98.9%; Pred. No. 4.2e-236;
Matches 647; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 MEENQNCIPYCNLSNPEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
Db 1 MEENQNCIPYCNLSNPEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
QY 61 DFVWGIQVPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKEWEDP 120

Db 61 DFVWGIQVPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKEWEDP 120
QY 121 NNPAATRTVIDRFRILDLGLLDRDIPSFRISSGEVPLLSVYAAQANLHLAILRDSVIFGR 180
Db 121 NNPAATRTVIDRFRILDLGLLDRDIPSFRISSGEVPLLSVYAAQANLHLAILRDSVIFGR 180
QY 181 WGLTTINVENYNNRLIRHIDEYADHCANTYRGLNPLKSTYQDMWITYNRLRDLTLTVL 240
Db 181 WGLTTINVENYNNRLIRHIDEYADHCANTYRGLNPLKSTYQDMWITYNRLRDLTLTVL 240
QY 241 DIAAFPPNNDNRYPYQPVGQLTRVYTDPLINFPQLQSVLAQLPTFNWESSAIRNPHL 300
Db 241 DIAAFPPNNDNRYPYQPVGQLTRVYTDPLINFPQLQSVLAQLPTFNWESSAIRNPHL 300
QY 301 FDLNNLTITFTDFSGVGRFPGCHRVISLIGCGNITSPIYGRANQBPSPFTFNGPV 360
Db 301 FDLNNLTITFTDFSGVGRFPGCHRVISLIGCGNITSPIYGRANQBPSPFTFNGPV 360
QY 361 FRTLSPITLRLLOQPCORHFNLRGEGVEFSTPTNSFTYRGRTVDSLTLPEDNSVP 420
Db 361 FRTLSPITLRLLOQPCORHFNLRGEGVEFSTPTNSFTYRGRTVDSLTLPEDNSVP 420
QY 421 PREGYSHRLCHATFVQSGTPTLTTGVVFSWTHRSATLNTIDPERINOIPLVKGRVWG 480
Db 421 PREGYSHRLCHATFVQSGTPTLTTGVVFSWTHRSATLNTIDPERINOIPLVKGRVWG 480
QY 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNSPITQRYLRFYASSRDARVILVTGAA 540
Db 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNSPITQRYLRFYASSRDARVILVTGAA 540
QY 541 STVGGOVSVNMPLOKTMIEGNLTSRTFRYTDPSNPPSFRANPDIIIGISEQPLFCAGSI 600
Db 541 STVGGOVSVNMPLOKTMIEGNLTSRTFRYTDPSNPPSFRANPDIIIGISEQPLFCAGSI 600
QY 601 SSGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNOIGLKTVDYHID 654
Db 601 SSGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNOIGLKTVDYHID 654

RESULT 5
A37829
parasporal crystal protein cryIaI - Bacillus thuringiensis
C.Species: Bacillus thuringiensis
C.Date: 14-Jun-1991 #sequence_revision 03-May-1994 #text_change 01-Dec-2000
C.Accession: A37829; S13762; S14438
R.Visser, B.; Munsterman, E.; Stoker, A.; Dirkse, W.G.
J. Bacteriol. 172, 6783-6788, 1990
A.Title: A novel Bacillus thuringiensis gene encoding a Spodoptera exigua-specific cryI
A.Reference number: A37829; MUID:91072224; PMID:2254254
A.Accession: A37829
A.Molecule type: DNA
A.Residues: 1-1171 <VI2>
A.Cross-references: EMBL:X53985
A.Note: translation is incomplete
C.Superfamily: parasporal crystal protein
C.Keywords: delta-endotoxin

Query Match 61.5%; Score 2680; DB 2; Length 1171;
Best Local Similarity 64.5%; Pred. No. 2e-185;
Matches 536; Conservative 88; Mismatches 169; Indels 38; Gaps 15;

QY 4 NNQNCIPYCNLSNPEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLIDF 62
Db 5 NNQNCIPYCNLSNPEVLLDIER---SNSVTATNIALEISRLASATPIGIGLILGFLPA 61
QY 63 VWGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKEWEDPNN 122
Db 62 IWGIGPSQWDLFLEQIELLDQKIEEFARNAQISRLSGISLYGIYTEAFREWEADPTN 121
QY 123 PATRTVIDRFRILDLGLLDRDIPSFRISSGEVPLLSVYAAQANLHLAILRDSVIFGR 182
Db 122 PALKEEMRTQPDNDMSILVTAIPLFVSQVQVPLFVSVAQANLHSLVLRDVSFVGQAWG 181

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OM protein - protein search, using sw model

Run on: October 9, 2003, 13:22:04 ; Search time 32 Seconds
(without alignments)
1088.182 Million cell updates/sec

Title: US-09-918-485-2
Perfect score: 4358
Sequence: 1 MEENNONQICIPYNCLSNPBE.....GEPNRCAPHEWNPDLDCSC 823

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4358	100.0	823	1	US-08-461-551-2
2	4358	100.0	823	4	US-09-037-621A-2
3	4294	98.5	1189	6	5188960-6
4	4289	98.4	1189	1	US-08-602-737-2
5	4289	98.4	1189	2	US-08-980-071-12
6	4289	98.4	1189	2	US-08-757-536-12
7	4289	98.4	1189	3	US-09-314-093-12
8	4289	98.4	1189	3	US-09-250-848-12
9	4289	98.4	1189	3	US-09-251-885-12
10	4289	98.4	1189	3	US-09-001-982-2
11	4289	98.4	1189	4	US-09-337-635-12
12	4289	98.4	1189	4	US-09-337-280-12
13	4288	98.4	1189	1	US-07-828-788A-16
14	4288	98.4	1189	1	US-08-356-034-6
15	4288	98.4	1189	2	US-08-980-071-2
16	4288	98.4	1189	2	US-08-980-071-6
17	4288	98.4	1189	2	US-08-757-536-2
18	4288	98.4	1189	2	US-08-757-536-6
19	4288	98.4	1189	3	US-09-314-093-2
20	4288	98.4	1189	3	US-09-314-093-6
21	4288	98.4	1189	3	US-08-933-891-6
22	4288	98.4	1189	3	US-09-250-848-2
23	4288	98.4	1189	3	US-09-250-848-6
24	4288	98.4	1189	3	US-09-251-885-2
25	4288	98.4	1189	3	US-09-251-885-6
26	4288	98.4	1189	4	US-09-337-635-2
27	4288	98.4	1189	4	US-09-337-635-6

28	4288	98.4	1189	4	US-09-337-280-2	Sequence 2, Appli
29	4288	98.4	1189	4	US-09-337-280-6	Sequence 6, Appli
30	4288	98.4	1189	4	US-09-521-344-6	Sequence 6, Appli
31	4288	98.4	1189	5	PCT-US92-11337-16	Sequence 16, Appli
32	4287	98.4	1189	2	US-08-980-071-4	Sequence 4, Appli
33	4287	98.4	1189	2	US-08-757-536-4	Sequence 4, Appli
34	4287	98.4	1189	3	US-09-314-093-4	Sequence 4, Appli
35	4287	98.4	1189	3	US-09-250-848-4	Sequence 4, Appli
36	4287	98.4	1189	3	US-09-251-885-4	Sequence 4, Appli
37	4287	98.4	1189	4	US-09-337-635-4	Sequence 4, Appli
38	4287	98.4	1189	4	US-09-337-280-4	Sequence 4, Appli
39	4283	98.3	1189	2	US-08-980-071-10	Sequence 10, Appli
40	4283	98.3	1189	2	US-08-757-536-10	Sequence 10, Appli
41	4283	98.3	1189	3	US-09-314-093-10	Sequence 10, Appli
42	4283	98.3	1189	3	US-09-250-848-10	Sequence 10, Appli
43	4283	98.3	1189	3	US-09-251-885-10	Sequence 10, Appli
44	4283	98.3	1189	4	US-09-337-635-10	Sequence 10, Appli
45	4283	98.3	1189	4	US-09-337-280-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1

US-08-461-551-2
; Sequence 2, Application US/08461551
; Patent No. 5792928

GENERAL INFORMATION:

APPLICANT: SANCHIS, Vincent
APPLICANT: LERECLOS, Didier
APPLICANT: MENOU, Ghislaine
APPLICANT: LECADET, Marguerite-Marie
APPLICANT: MARTOURET, Daniel
APPLICANT: DEPONDER, Raymond

TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR

TITLE OF INVENTION: POLYPEPTIDES ENDOWED WITH A LARVICIDAL ACTIVITY TOWARDS

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS: 2

ADDRESSER: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22313

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,551
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,652
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/458,754
FILING DATE: 11-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 88 401 121.4
FILING DATE: 06-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 87 08090
FILING DATE: 10-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: HUNTINGTON, R. D.
REGISTRATION NUMBER: 27,903
REFERENCE/DOCKET NUMBER: 010830-073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021

Patent No. 6310035
GENERAL INFORMATION:
APPLICANT: SANCHIS, Vincent
LERECLUS, Didier
MENOU, Ghislaine
LECADET, Marguerite-Marie
MARTOURET, Daniel
DEDONDER, Raymond
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR
POLYPEPTIDES ENDOWED WITH A LARVICIDAL ACTIVITY TOWARDS
LEPIDOPTERA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,621A
FILING DATE: 10-Mar-1998
CLASSIFICATION: <Unknown>
11-DEC-1989
06-MAY-1988
10-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,551
FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/458,754
FILING DATE: 11-DEC-1989
APPLICATION NUMBER: EP 88 401 121.4
FILING DATE: 06-MAY-1988
APPLICATION NUMBER: FR 87 08090
FILING DATE: 10-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: HUNTINGTON, R. D.
REGISTRATION NUMBER: 27,903
REFERENCE/DOCKET NUMBER: 010830-073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 823 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-037-621A-2
Query Match 100.0%; Score 4358; DB 1; Length 823;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEENNQOCIPYCNLSNPEVLDDGERISTGSSIDISLSVQPLVSNFVPGGFLVGLI 60
DB 1 MEENNQOCIPYCNLSNPEVLDDGERISTGSSIDISLSVQPLVSNFVPGGFLVGLI 60
QY 61 DFVWGIQVPSQWDAFLVQIEQLINERIAEFARNAATANLEGLGNFNIVVEAFKEWEDP 120
DB 61 DFVWGIQVPSQWDAFLVQIEQLINERIAEFARNAATANLEGLGNFNIVVEAFKEWEDP 120
QY 121 NNPATRTRVIDRFRILDLGLERDIPFRISGFVEPLLSVYQAANHLALRDSVIFGER 180
DB 121 NNPATRTRVIDRFRILDLGLERDIPFRISGFVEPLLSVYQAANHLALRDSVIFGER 180
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 823 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-037-621A-2
Query Match 100.0%; Score 4358; DB 1; Length 823;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MEENNQOCIPYCNLSNPEVLDDGERISTGSSIDISLSVQPLVSNFVPGGFLVGLI 60
QY 61 DFVWGIQVPSQWDAFLVQIEQLINERIAEFARNAATANLEGLGNFNIVVEAFKEWEDP 120
DB 61 DFVWGIQVPSQWDAFLVQIEQLINERIAEFARNAATANLEGLGNFNIVVEAFKEWEDP 120
QY 121 NNPATRTRVIDRFRILDLGLERDIPFRISGFVEPLLSVYQAANHLALRDSVIFGER 180
DB 121 NNPATRTRVIDRFRILDLGLERDIPFRISGFVEPLLSVYQAANHLALRDSVIFGER 180
US-08-461-551-2
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MEENNQOCIPYCNLSNPEVLDDGERISTGSSIDISLSVQPLVSNFVPGGFLVGLI 60
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DB 61 DFVWGIQVPSQWDAFLVQIEQLINERIAEFARNAATANLEGLGNFNIVVEAFKEWEDP 120
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DB 121 NNPATRTRVIDRFRILDLGLERDIPFRISGFVEPLLSVYQAANHLALRDSVIFGER 180
QY 181 WGLTTINVENYRLRHHIDEYADHCANTYNGIANLKPSTYQDMITYNLRDLTLVL 240
DB 181 WGLTTINVENYRLRHHIDEYADHCANTYNGIANLKPSTYQDMITYNLRDLTLVL 240
QY 241 DIAAFPPYDNRYPYQPVQQLTRVYTDPLINFNQLOSVQALPTFNWESSATRNPHL 300
DB 241 DIAAFPPYDNRYPYQPVQQLTRVYTDPLINFNQLOSVQALPTFNWESSATRNPHL 300
QY 301 FDLANLAIPTDFWESVGRNRYFYGWHRVYSSIGGNITSPYIGREANQEPFRFTFNGV 360
DB 301 FDLANLAIPTDFWESVGRNRYFYGWHRVYSSIGGNITSPYIGREANQEPFRFTFNGV 360
QY 361 FRTLSIPTLRLLQPCORHFNLRGEGVEFTPTNSFTYRGRTVDSLTTELPPDNSVP 420
DB 361 FRTLSIPTLRLLQPCORHFNLRGEGVEFTPTNSFTYRGRTVDSLTTELPPDNSVP 420
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DB 421 PRGYSHRLCHATFQVRSQTPFTLTGTVFVSWTHRSATLNTIDPERINQPLVKGFRVWG 480
QY 481 GTSVITGPGFTGGDLRRNTFGDFVSLQVNSPITQRYELFRYASSRDARVILTGAA 540
DB 481 GTSVITGPGFTGGDLRRNTFGDFVSLQVNSPITQRYELFRYASSRDARVILTGAA 540
QY 541 STGVGQVSNVNPLOKMEIGENLTSTRTYDFSNPFSFRANPDIIGISQPLFGAGSI 600
DB 541 STGVGQVSNVNPLOKMEIGENLTSTRTYDFSNPFSFRANPDIIGISQPLFGAGSI 600
QY 601 SSGELYIDKIEILLADATFEASDLERAQAVNALFTSSNOIGLKTVDVTHIDQVSNLV 660
DB 601 SSGELYIDKIEILLADATFEASDLERAQAVNALFTSSNOIGLKTVDVTHIDQVSNLV 660
QY 661 DCLSDFCDEKRELSEKVGAKLSDEENLQDNPERGNINQPDGWRGSTDITIOGGD 720
DB 661 DCLSDFCDEKRELSEKVGAKLSDEENLQDNPERGNINQPDGWRGSTDITIOGGD 720
QY 721 DVFKENVTLPQTVDECYPTLYQKIDESKLYAYTRVELGYIEDSDLEIYLLAYNAKH 780
DB 721 DVFKENVTLPQTVDECYPTLYQKIDESKLYAYTRVELGYIEDSDLEIYLLAYNAKH 780
QY 781 EIVNVPGTGLMPLSAQSPICKGCEPNRCAPHLEWNPDLDCSC 823
DB 781 EIVNVPGTGLMPLSAQSPICKGCEPNRCAPHLEWNPDLDCSC 823
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US-09-037-621A-2
; Sequence 2, Application us/09037621a

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 Db 181 WGLTTINVENNRLIRHIDEYADHCANTYNGRLNLPKSTYQDWITYNRLRDLTLTVL 240
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 Db 241 DIAAFFPNYDNRYPQPVQQLTREYVTDPLINFNPOLQSVQALPTFNWESSAIRNPHL 300
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 Db 301 FDIANNLTFTDWFSGRNFYMGHVRVSSLLGGNITSPITYGREANQEPFRFTNGPV 360
 QY 361 FRTLSIPTLRLLQOQPCORHHFNLRGEGVEFSTPTNSFTYRGRTVDSLTELPPEDNSVP 420
 Db 361 FRTLSIPTLRLLQOQPCORHHFNLRGEGVEFSTPTNSFTYRGRTVDSLTELPPEDNSVP 420
 QY 421 PREGYSHRLCHATFVQSGTPTLTGVPFWSWTHRSATLTNTIDPERINQIPLVKGFRVMG 480
 Db 421 PREGYSHRLCHATFVQSGTPTLTGVPFWSWTHRSATLTNTIDPERINQIPLVKGFRVMG 480
 QY 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNSPITQRYELRFRYASSRDARVIVLTGAA 540
 Db 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNSPITQRYELRFRYASSRDARVIVLTGAA 540
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 Db 541 STGVGGQSVNMPLOKTMIEGENLTSTRPTRYTDFSNPFSFRANPDIIGISEQPLFCAGSI 600
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 Db 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNOIGLKTVDYDHYDQVSNLV 660
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 Db 661 DCLSBDFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGWSGTDTITIQGGD 720
 QY 721 DVFENYVTLPGTVDECYPTLYQKIDESKLYATRYELRGYIEDSQDLEIYLAIYNAKH 780
 Db 721 DVFENYVTLPGTVDECYPTLYQKIDESKLYATRYELRGYIEDSQDLEIYLAIYNAKH 780
 QY 781 EIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
 Db 781 EIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 3

5188960-6
 ; Patent No. 5188960
 ; APPLICANT: PAYNE, JEWEL, SICK, AUGUST J.
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATE ACTIVE
 ; AGAINST LEPIDOPTERAN PESTS, AND GENES ENCODING NOVEL
 ; LEPIDOPTERAN-ACTIVE TOXINS
 ; NUMBER OF SEQUENCES: 8
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/451,261
 ; FILING DATE: 14-DEC-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 371,955
 ; FILING DATE: 27-JUN-1989
 ; SEQ ID NO: 6:
 ; LENGTH: 1189
 5188960-6

Query Match 98.5%; Score 4294; DB 6; Length 1189;
 Best Local Similarity 99.0%; Pred. No. 0;
 Matches 815; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 MEENNQCPYNCLSNPEVLLDGERISTGNSSIDISLVQFLVSNFVPGGFLVGLI 60
 Db 1 MEENNQCPYNCLSNPEVLLDGERISTGNSSIDISLVQFLVSNFVPGGFLVGLI 60
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Db 61 DFWGIVGSPQDWAFLVQIEQLINERIAFARNAAIANLEGNNFNIIYVEAFKWEEDP 120
 QY 121 NNPAFTRVIDFRILDGLLERDIPSGFRISGPEVPLLSVVAQANLHLAILRDSVIFGER 180
 Db 121 NNPAFTRVIDFRILDGLLERDIPSGFRISGPEVPLLSVVAQANLHLAILRDSVIFGER 180
 QY 181 WGLTTINVENNRLIRHIDEYADHCANTYNGRLNLPKSTYQDWITYNRLRDLTLTVL 240
 Db 181 WGLTTINVENNRLIRHIDEYADHCANTYNGRLNLPKSTYQDWITYNRLRDLTLTVL 240
 QY 241 DIAAFFPNYDNRYPQPVQQLTREYVTDPLINFNPOLQSVQALPTFNWESSAIRNPHL 300
 Db 241 DIAAFFPNYDNRYPQPVQQLTREYVTDPLINFNPOLQSVQALPTFNWESSAIRNPHL 300
 QY 301 FDIANNLTFTDWFSGRNFYMGHVRVSSLLGGNITSPITYGREANQEPFRFTNGPV 360
 Db 301 FDIANNLTFTDWFSGRNFYMGHVRVSSLLGGNITSPITYGREANQEPFRFTNGPV 360
 QY 361 FRTLSIPTLRLLQOQPCORHHFNLRGEGVEFSTPTNSFTYRGRTVDSLTELPPEDNSVP 420
 Db 361 FRTLSIPTLRLLQOQPCORHHFNLRGEGVEFSTPTNSFTYRGRTVDSLTELPPEDNSVP 420
 QY 421 PREGYSHRLCHATFVQSGTPTLTGVPFWSWTHRSATLTNTIDPERINQIPLVKGFRVMG 480
 Db 421 PREGYSHRLCHATFVQSGTPTLTGVPFWSWTHRSATLTNTIDPERINQIPLVKGFRVMG 480
 QY 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNSPITQRYELRFRYASSRDARVIVLTGAA 540
 Db 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNSPITQRYELRFRYASSRDARVIVLTGAA 540
 QY 541 STGVGGQSVNMPLOKTMIEGENLTSTRPTRYTDFSNPFSFRANPDIIGISEQPLFCAGSI 600
 Db 541 STGVGGQSVNMPLOKTMIEGENLTSTRPTRYTDFSNPFSFRANPDIIGISEQPLFCAGSI 600
 QY 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNOIGLKTVDYDHYDQVSNLV 660
 Db 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNOIGLKTVDYDHYDQVSNLV 660
 QY 661 DCLSBDFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGWSGTDTITIQGGD 720
 Db 661 DCLSBDFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGWSGTDTITIQGGD 720
 QY 721 DVFENYVTLPGTVDECYPTLYQKIDESKLYATRYELRGYIEDSQDLEIYLAIYNAKH 780
 Db 721 DVFENYVTLPGTVDECYPTLYQKIDESKLYATRYELRGYIEDSQDLEIYLAIYNAKH 780
 QY 781 EIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
 Db 781 EIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 4

US-08-602-737-2
 ; Sequence 2, Application US/08602737
 ; Patent No. 5736131
 ; GENERAL INFORMATION:
 ; APPLICANT: Bosch, Hendrick J
 ; APPLICANT: Stiekema, Willem J
 ; TITLE OF INVENTION: Hybrid Toxin
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SANDOZ AGRO, INC
 ; STREET: 975 California Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: CA 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:

us-09-918-485-2.ra1

Wed Oct 15 11:56:18 2003

APPLICATION NUMBER: US/08/602,737
FILING DATE: 21-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Marcus-Wyner, Lynn
REGISTRATION NUMBER: 34,869
REFERENCE/DOCKET NUMBER: 130-4080
TELEPHONE: 415-354-3588
TELEFAX: 415-857-1125
INFORMATION FOR SEQ ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-602-737-2

Query Match 98.4%; Score 4289; DB 1; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 MEENNQCIPYCLNPEEVLDDGERISTGNSIDISLSVQLVSNFVPGGGLVGLI 60
DB 1 MEENNQCIPYCLNPEEVLDDGERISTGNSIDISLSVQLVSNFVPGGGLVGLI 60
QY 61 DFVWGIQPSQWDAFLVQIEQLINERIAEPARNAATANLEGLGNFNLYVEAFKEWEDP 120
DB 61 DFVWGIQPSQWDAFLVQIEQLINERIAEPARNAATANLEGLGNFNLYVEAFKEWEDP 120
QY 121 NNPAATRTVIDRFRILDGLLDRDIPSPRISGFVPLLSVYQAANLHAILRDSVIFGER 180
DB 121 NNPAATRTVIDRFRILDGLLDRDIPSPRISGFVPLLSVYQAANLHAILRDSVIFGER 180
QY 181 WGLTTINNVNENYRLIRHIDEVADHCANTYRNLNLPKSTYQDMITYNRLRDLTLTVL 240
DB 181 WGLTTINNVNENYRLIRHIDEVADHCANTYRNLNLPKSTYQDMITYNRLRDLTLTVL 240
QY 241 DIAAFPNYDNRYPIDPVGQLTREVTYDPLNPNQVLSVQLVSNFVPGGGLVGLI 300
DB 241 DIAAFPNYDNRYPIDPVGQLTREVTYDPLNPNQVLSVQLVSNFVPGGGLVGLI 300
QY 301 FDLANNLTFTDWFSGVGRNFYMGHVRVSSLIIGGNTSPYIGREANQEPFRSFTNGVP 360
DB 301 FDLANNLTFTDWFSGVGRNFYMGHVRVSSLIIGGNTSPYIGREANQEPFRSFTNGVP 360
QY 361 FRLTSLPTLRLLQCPQCORHHNLRGEGVEFTPTNSFTYRGRGTVDLSLTLPEDNSVP 420
DB 361 FRLTSLPTLRLLQCPQCORHHNLRGEGVEFTPTNSFTYRGRGTVDLSLTLPEDNSVP 420
QY 421 PRGYSHRLCHATFVQSGTPELTTCGVFSTHRSATLTNTIDPERINQIPLVKGFRVWG 480
DB 421 PRGYSHRLCHATFVQSGTPELTTCGVFSTHRSATLTNTIDPERINQIPLVKGFRVWG 480
QY 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNSPTORVBLRFRVASSRDARVILTGAA 540
DB 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNSPTORVBLRFRVASSRDARVILTGAA 540
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QY 661 DCLDFECFLDEKRELSEKVKIAKLSDERNLLQDPNFRGINRQPDGRGSGTDTIQGGD 720
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QY 721 DVFENKVVTLPGTVDECYPTLYQKIDESKIKAYTRYELRGYIEDSDQLEIYLIAYNKX 780
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781 EIVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
781 EIVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 5
US-08-980-071-12 Application US/08980071
Sequence 12, Patent No. 5914318
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Gilmer, Amy Jelen
APPLICANT: Metcalf, Anne-Marie Light
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
TITLE OF INVENTION: LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,071
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/757,536
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO. 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-980-071-12

Query Match 98.4%; Score 4289; DB 2; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 MEENNQCIPYCLNPEEVLDDGERISTGNSIDISLSVQLVSNFVPGGGLVGLI 60
DB 1 MEENNQCIPYCLNPEEVLDDGERISTGNSIDISLSVQLVSNFVPGGGLVGLI 60
QY 61 DFVWGIQPSQWDAFLVQIEQLINERIAEPARNAATANLEGLGNFNLYVEAFKEWEDP 120
DB 61 DFVWGIQPSQWDAFLVQIEQLINERIAEPARNAATANLEGLGNFNLYVEAFKEWEDP 120
QY 121 NNPAATRTVIDRFRILDGLLDRDIPSPRISGFVPLLSVYQAANLHAILRDSVIFGER 180
DB 121 NNPAATRTVIDRFRILDGLLDRDIPSPRISGFVPLLSVYQAANLHAILRDSVIFGER 180
QY 181 WGLTTINNVNENYRLIRHIDEVADHCANTYRNLNLPKSTYQDMITYNRLRDLTLTVL 240
DB 181 WGLTTINNVNENYRLIRHIDEVADHCANTYRNLNLPKSTYQDMITYNRLRDLTLTVL 240
QY 241 DIAAFPNYDNRYPIDPVGQLTREVTYDPLNPNQVLSVQLVSNFVPGGGLVGLI 300

Db 241 DIAFFPNYNNRRYPQPVQQLTRVYTDPLINFPOLQSVQALPTFNWESSAIRNPHL 300
Qy 301 FDILNNLTITDWFSGVGRNFWGHRVVISSILGCGNITSPIYGREANQEPSPRFTNGPV 360
Db 301 FDILNNLTITDWFSGVGRNFWGHRVVISSILGCGNITSPIYGREANQEPSPRFTNGPV 360
Qy 361 FRTLSTPTLLLOQPQPCORHHFNLRGGECVFPSTPNSFTYRGRGTWDSLTLPEDNSVP 420
Db 361 FRTLSTPTLLLOQPQPCORHHFNLRGGECVFPSTPNSFTYRGRGTWDSLTLPEDNSVP 420
Qy 421 PREGYSHRLCHATFVQSRGTPPLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
Db 421 PREGYSHRLCHATFVQSRGTPPLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
Qy 481 GTSVITGPGTGDILARNFTGDFVSLQVNNINSPIQRYELRFRYASSRDARVIVLTGAA 540
Db 481 GTSVITGPGTGDILARNFTGDFVSLQVNNINSPIQRYELRFRYASSRDARVIVLTGAA 540
Qy 541 STGVGGQSVNMPLOKTMELGENLTSTRTFRYTDPSNPFSPRANPDIIGISEQPLFGAGSI 600
Db 541 STGVGGQSVNMPLOKTMELGENLTSTRTFRYTDPSNPFSPRANPDIIGISEQPLFGAGSI 600
Qy 601 SSGELYIDKIEIILADATPEASDLERAQAKAVNALFTSSNQIGLKTVDYHIDQVSNLV 660
Db 601 SSGELYIDKIEIILADATPEASDLERAQAKAVNALFTSSNQIGLKTVDYHIDQVSNLV 660
Qy 661 DCLSDFCLEKRELSKVKHAKRLSDERNLLQDPNFRGINRQPDGRGSGTDITIQGGD 720
Db 661 DCLSDFCLEKRELSKVKHAKRLSDERNLLQDPNFRGINRQPDGRGSGTDITIQGGD 720
Qy 721 DVFKNYVTLPGTVDECYPTLYQKIDESKLYATRYELRGYTEDSQDLEIYLIRYNAKH 780
Db 721 DVFKNYVTLPGTVDECYPTLYQKIDESKLYATRYELRGYTEDSQDLEIYLIRYNAKH 780
Qy 781 EIVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
Db 781 EIVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 6
US-08-757-536-12
; Sequence 12, Application US/08757536
; Patent No. 5942664
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Gilmer, Amy Jelen
; APPLICANT: Mettus, Anne-Marie Light
; TITLE OF INVENTION: Bacillus thuringiensis Cryic
; TITLE OF INVENTION: Compositions Toxic to Lepidopteran Insects and Methods for
; TITLE OF INVENTION: Making Cryic Mutants
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White and Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,536
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MOBT-023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1189 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-757-536-12

Query Match 98.4%; Score 4289; DB 2; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MEENNONQICIPNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
Db 1 MEENNONQICIPNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
Qy 61 DFWGIVGSPQWDALVQIEQLINERIAEFARNAAIANLEGNNFNIIYVEAFKWEEDP 120
Db 61 DFWGIVGSPQWDALVQIEQLINERIAEFARNAAIANLEGNNFNIIYVEAFKWEEDP 120
Qy 121 NNPAATRTVIDRFRILDLGLERDIPSFRIISGEFVPLSVYAAANLHLAIRDVSIFGER 180
Db 121 NNPAATRTVIDRFRILDLGLERDIPSFRIISGEFVPLSVYAAANLHLAIRDVSIFGER 180
Qy 181 WGLTTINNVNENYRLIRIHIDEVADHCANTYRGLNANLPSKTYQDMITYNRLRDLTLTVL 240
Db 181 WGLTTINNVNENYRLIRIHIDEVADHCANTYRGLNANLPSKTYQDMITYNRLRDLTLTVL 240
Qy 241 DIAAFPNYNNRRYPQPVQQLTRVYTDPLINFPOLQSVQALPTFNWESSAIRNPHL 300
Db 241 DIAAFPNYNNRRYPQPVQQLTRVYTDPLINFPOLQSVQALPTFNWESSAIRNPHL 300
Qy 301 FDILNNLTITDWFSGVGRNFWGHRVVISSILGCGNITSPIYGREANQEPSPRFTNGPV 360
Db 301 FDILNNLTITDWFSGVGRNFWGHRVVISSILGCGNITSPIYGREANQEPSPRFTNGPV 360
Qy 361 FRTLSTPTLLLOQPQPCORHHFNLRGGECVFPSTPNSFTYRGRGTWDSLTLPEDNSVP 420
Db 361 FRTLSTPTLLLOQPQPCORHHFNLRGGECVFPSTPNSFTYRGRGTWDSLTLPEDNSVP 420
Qy 421 PREGYSHRLCHATFVQSRGTPPLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
Db 421 PREGYSHRLCHATFVQSRGTPPLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
Qy 481 GTSVITGPGTGDILARNFTGDFVSLQVNNINSPIQRYELRFRYASSRDARVIVLTGAA 540
Db 481 GTSVITGPGTGDILARNFTGDFVSLQVNNINSPIQRYELRFRYASSRDARVIVLTGAA 540
Qy 541 STGVGGQSVNMPLOKTMELGENLTSTRTFRYTDPSNPFSPRANPDIIGISEQPLFGAGSI 600
Db 541 STGVGGQSVNMPLOKTMELGENLTSTRTFRYTDPSNPFSPRANPDIIGISEQPLFGAGSI 600
Qy 601 SSGELYIDKIEIILADATPEASDLERAQAKAVNALFTSSNQIGLKTVDYHIDQVSNLV 660
Db 601 SSGELYIDKIEIILADATPEASDLERAQAKAVNALFTSSNQIGLKTVDYHIDQVSNLV 660
Qy 661 DCLSDFCLEKRELSKVKHAKRLSDERNLLQDPNFRGINRQPDGRGSGTDITIQGGD 720
Db 661 DCLSDFCLEKRELSKVKHAKRLSDERNLLQDPNFRGINRQPDGRGSGTDITIQGGD 720
Qy 721 DVFKNYVTLPGTVDECYPTLYQKIDESKLYATRYELRGYTEDSQDLEIYLIRYNAKH 780
Db 721 DVFKNYVTLPGTVDECYPTLYQKIDESKLYATRYELRGYTEDSQDLEIYLIRYNAKH 780
Qy 781 EIVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
Db 781 EIVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 7
US-09-314-093-12
; Sequence 12, Application US/09314093

Patent No. 6033874
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Gilmer, Amy Jelen
APPLICANT: Mettus, Anne-Marie Light
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
TITLE OF INVENTION: LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/314,093
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/980,071
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-314-093-12

Query Match 98.4%; Score 4289; DB 3; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY	1	MEENNQCIPYNCLSNP	EVLLDGERISTGNS	SIDISLSVQFLVNSFVPGGFLVGLI	60
DB	1	MEENNQCIPYNCLSNP <td>EVLLDGERISTGNS<td>SIDISLSVQFLVNSFVPGGFLVGLI<td>60</td></td></td>	EVLLDGERISTGNS <td>SIDISLSVQFLVNSFVPGGFLVGLI<td>60</td></td>	SIDISLSVQFLVNSFVPGGFLVGLI <td>60</td>	60
QY	61	DFWGVGPSQWDAFLVQ <td>IBOLINERIAEFARNA</td> <td>ANLEGLGNFNFIYVEAFKEWEEDP</td> <td>120</td>	IBOLINERIAEFARNA	ANLEGLGNFNFIYVEAFKEWEEDP	120
DB	61	DFWGVGPSQWDAFLVQ <td>IBOLINERIAEFARNA</td> <td>ANLEGLGNFNFIYVEAFKEWEEDP</td> <td>120</td>	IBOLINERIAEFARNA	ANLEGLGNFNFIYVEAFKEWEEDP	120
QY	121	NPDATETVIDRFRILQ <td>LERDIPSRISGFEVPL<td>SVYQAANLHLAIRDSVIFGER</td><td>180</td></td>	LERDIPSRISGFEVPL <td>SVYQAANLHLAIRDSVIFGER</td> <td>180</td>	SVYQAANLHLAIRDSVIFGER	180
DB	121	NPDATETVIDRFRILQ <td>LERDIPSRISGFEVPL<td>SVYQAANLHLAIRDSVIFGER</td><td>180</td></td>	LERDIPSRISGFEVPL <td>SVYQAANLHLAIRDSVIFGER</td> <td>180</td>	SVYQAANLHLAIRDSVIFGER	180
QY	181	WGLTTINNVNENRILR <td>IDEVADHCANTYNGLN</td> <td>NLPKSTYQDMITYNLRRLDLTLVL</td> <td>240</td>	IDEVADHCANTYNGLN	NLPKSTYQDMITYNLRRLDLTLVL	240
DB	181	WGLTTINNVNENRILR <td>IDEVADHCANTYNGLN</td> <td>NLPKSTYQDMITYNLRRLDLTLVL</td> <td>240</td>	IDEVADHCANTYNGLN	NLPKSTYQDMITYNLRRLDLTLVL	240
QY	241	DIAAFPYNDNRPIQVQ <td>LREVTVDPLINFPOLQ</td> <td>SVACLPTFNWMESSAIRNPHL</td> <td>300</td>	LREVTVDPLINFPOLQ	SVACLPTFNWMESSAIRNPHL	300
DB	241	DIAAFPYNDNRPIQVQ <td>LREVTVDPLINFPOLQ</td> <td>SVACLPTFNWMESSAIRNPHL</td> <td>300</td>	LREVTVDPLINFPOLQ	SVACLPTFNWMESSAIRNPHL	300
QY	301	FDILNNLTFTDWFSG <td>RNVGCHRVISLSIGCN</td> <td>ITSYICVGRANQBPRESFTNGPV</td> <td>360</td>	RNVGCHRVISLSIGCN	ITSYICVGRANQBPRESFTNGPV	360
DB	301	FDILNNLTFTDWFSG <td>RNVGCHRVISLSIGCN</td> <td>ITSYICVGRANQBPRESFTNGPV</td> <td>360</td>	RNVGCHRVISLSIGCN	ITSYICVGRANQBPRESFTNGPV	360
QY	361	FRTLSIPTLRLLIQP	CQRHHFNLRGGEGVEF	STPTNFGTGRGTVDLSITELPEDNSVP	420
DB	361	FRTLSIPTLRLLIQP	CQRHHFNLRGGEGVEF	STPTNFGTGRGTVDLSITELPEDNSVP	420

QY	421	PREGYSHRLCHATEFV	QSGTPELTGTVVFSW	THRSATLNTNTIDPR	INQIPLVKGFRVWG	480
DB	421	PREGYSHRLCHATEFV	QSGTPELTGTVVFSW	THRSATLNTNTIDPR	INQIPLVKGFRVWG	480
QY	481	GTSVITGPGFTGGD	ILRRNTFGDFVSLQV	INSPIQRYLRLFRYAS	SRDARVIVLTGAA	540
DB	481	GTSVITGPGFTGGD	ILRRNTFGDFVSLQV	INSPIQRYLRLFRYAS	SRDARVIVLTGAA	540
QY	541	STGVGGQVSNVPLQK	MEIGENLTSRTFRYT	DFSNPFSFRANPDII	GISBQPLFGAGSI	600
DB	541	STGVGGQVSNVPLQK	MEIGENLTSRTFRYT	DFSNPFSFRANPDII	GISBQPLFGAGSI	600
QY	601	SSGELYDKIELILL	ADATPEAESDLERAK	AVNALFTSSNOIGLK	TDVTDYHIDQVSNLV	660
DB	601	SSGELYDKIELILL	ADATPEAESDLERAK	AVNALFTSSNOIGLK	TDVTDYHIDQVSNLV	660
QY	661	DCLSDPFLDKRELSE	KVGHAKRSDERNLLQ	DPNFRGINROPDRG	WRGSTDTITIOGGD	720
DB	661	DCLSDPFLDKRELSE	KVGHAKRSDERNLLQ	DPNFRGINROPDRG	WRGSTDTITIOGGD	720
QY	721	DVFKENYVTLPGTV	DECPYLYQKIDESKL	KATRYELRGYIEDSO	DLLEIYLAYNAKH	780
DB	721	DVFKENYVTLPGTV	DECPYLYQKIDESKL	KATRYELRGYIEDSO	DLLEIYLAYNAKH	780
QY	781	EIVNVFCTGSLWPL	SAQSPIGKCGEPNRC	APHLEWNPDLCSC	823	
DB	781	EIVNVFCTGSLWPL	SAQSPIGKCGEPNRC	APHLEWNPDLCSC	823	

RESULT 8
US-09-250-848-12
Sequence 12, Application US/09250848
Patent No. 6153814
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Gilmer, Amy Jelen
APPLICANT: Mettus, Anne-Marie Light
TITLE OF INVENTION: Bacillus thuringiensis Cry1C
TITLE OF INVENTION: Compositions Toxic to Lepidopteran Insects and Methods for
TITLE OF INVENTION: Making Cry1C Mutants
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White and Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/250,848
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/757,536
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOST:023
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-250-848-12

Query Match 98.4%; Score 4289; DB 3; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 MEENNQCIPIYNCISNPEVLLDGERISTGNSIDISLSVQFLVSNFVPGGFLVGLI 60
DB 1 MEENNQCIPIYNCISNPEVLLDGERISTGNSIDISLSVQFLVSNFVPGGFLVGLI 60

QY 61 DFVWGVGPSQWDAFLVQIOLINERIAEFARNAAIANLEGLNENFIYVEAFKEWEDP 120
DB 61 DFVWGVGPSQWDAFLVQIOLINERIAEFARNAAIANLEGLNENFIYVEAFKEWEDP 120

QY 121 NNPATRTRVIDRFRILDLGLERDIPSRISGFEVPLLSVYQAANLHLALRDSVIFGER 180
DB 121 NNPATRTRVIDRFRILDLGLERDIPSRISGFEVPLLSVYQAANLHLALRDSVIFGER 180

QY 181 WGLTTINVENNRLIRHIDEYADHCANTYRGLNLPKSTYQDWITYNRLRDLTLTVL 240
DB 181 WGLTTINVENNRLIRHIDEYADHCANTYRGLNLPKSTYQDWITYNRLRDLTLTVL 240

QY 241 DIAAFPNYDNRYPPIQPVQQLTREYVTDPLINFPOLQSVQALPTFNWESSAIRNPHL 300
DB 241 DIAAFPNYDNRYPPIQPVQQLTREYVTDPLINFPOLQSVQALPTFNWESSAIRNPHL 300

QY 301 FDIILNLTITDWFSGVGRNFWGHRVVISLIGGNITSPYIGREANQBPFRFTFNGPV 360
DB 301 FDIILNLTITDWFSGVGRNFWGHRVVISLIGGNITSPYIGREANQBPFRFTFNGPV 360

QY 361 FRTLSIPTLRLLQOQCORHHFNLRGGEGVEFSTPTNSFTYRGRTVDSLTELPPEDNSVP 420
DB 361 FRTLSIPTLRLLQOQWAPPNLRGVEGVEFSTPTNSFTYRGRTVDSLTELPPEDNSVP 420

QY 421 PREGYSHRLCHATFVQRSGTPELTGTVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
DB 421 PREGYSHRLCHATFVQRSGTPELTGTVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480

QY 481 GTSVITGPGTGGDILRRNTFGFVSLQVNNINSPIQRYRLRFRYASSRDARVILTGAA 540
DB 481 GTSVITGPGTGGDILRRNTFGFVSLQVNNINSPIQRYRLRFRYASSRDARVILTGAA 540

QY 541 STGVGGQVSNMPLQKTMIEGENLTGRTPTDPSNPPFRANPDIIIGISEQLFGAGSI 600
DB 541 STGVGGQVSNMPLQKTMIEGENLTGRTPTDPSNPPFRANPDIIIGISEQLFGAGSI 600

QY 601 SSGELYIDKIEIILADATPAESDLERAQKAVNALFTSSNQIGLKTVDYTHIDQVSNLV 660
DB 601 SSGELYIDKIEIILADATPAESDLERAQKAVNALFTSSNQIGLKTVDYTHIDQVSNLV 660

QY 661 DCLSDFECLDEKELSEKVKHAKRLDERNLLODPNFRGINRQPDGRWGSDTITIQGGD 720
DB 661 DCLSDFECLDEKELSEKVKHAKRLDERNLLODPNFRGINRQPDGRWGSDTITIQGGD 720

QY 721 DVPKENYVTLPGTVDECPYLYQKIDESKLAATRYELAGYIEDSQDLEIYLIYNAXH 780
DB 721 DVPKENYVTLPGTVDECPYLYQKIDESKLAATRYELAGYIEDSQDLEIYLIYNAXH 780

QY 781 EIVNVPGTSLWPLSAQSPKCGBNRCAPHLEWNPDLDCSC 823
DB 781 EIVNVPGTSLWPLSAQSPKCGBNRCAPHLEWNPDLDCSC 823

RESULT 9

US-09-251-885-12
Sequence 12, Application US/09251885
Patent No. 6177615
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Gilmer, Amy Jelen
APPLICANT: Mettus, Anne-Marie Light
TITLE OF INVENTION: Bacillus thuringiensis CryIc

TITLE OF INVENTION: Compositions Toxic to Lepidopteran Insects and Methods for
TITLE OF INVENTION: Making CryIc Mutants
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White and Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/251,885
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/757,536
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-251-885-12

Query Match 98.4%; Score 4289; DB 3; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 MEENNQCIPIYNCISNPEVLLDGERISTGNSIDISLSVQFLVSNFVPGGFLVGLI 60
DB 1 MEENNQCIPIYNCISNPEVLLDGERISTGNSIDISLSVQFLVSNFVPGGFLVGLI 60

QY 61 DFVWGVGPSQWDAFLVQIOLINERIAEFARNAAIANLEGLNENFIYVEAFKEWEDP 120
DB 61 DFVWGVGPSQWDAFLVQIOLINERIAEFARNAAIANLEGLNENFIYVEAFKEWEDP 120

QY 121 NNPATRTRVIDRFRILDLGLERDIPSRISGFEVPLLSVYQAANLHLALRDSVIFGER 180
DB 121 NNPATRTRVIDRFRILDLGLERDIPSRISGFEVPLLSVYQAANLHLALRDSVIFGER 180

QY 181 WGLTTINVENNRLIRHIDEYADHCANTYRGLNLPKSTYQDWITYNRLRDLTLTVL 240
DB 181 WGLTTINVENNRLIRHIDEYADHCANTYRGLNLPKSTYQDWITYNRLRDLTLTVL 240

QY 241 DIAAFPNYDNRYPPIQPVQQLTREYVTDPLINFPOLQSVQALPTFNWESSAIRNPHL 300
DB 241 DIAAFPNYDNRYPPIQPVQQLTREYVTDPLINFPOLQSVQALPTFNWESSAIRNPHL 300

QY 301 FDIILNLTITDWFSGVGRNFWGHRVVISLIGGNITSPYIGREANQBPFRFTFNGPV 360
DB 301 FDIILNLTITDWFSGVGRNFWGHRVVISLIGGNITSPYIGREANQBPFRFTFNGPV 360

QY 361 FRTLSIPTLRLLQOQCORHHFNLRGGEGVEFSTPTNSFTYRGRTVDSLTELPPEDNSVP 420
DB 361 FRTLSIPTLRLLQOQWAPPNLRGVEGVEFSTPTNSFTYRGRTVDSLTELPPEDNSVP 420

QY 421 PREGYSHRLCHATFVQRSGTPELTGTVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
DB 421 PREGYSHRLCHATFVQRSGTPELTGTVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480

QY 481 GTSVITGPGTGGDILRNTFGDVSLOVNSPITQRYRLFRYASSDARVILTGAA 540
DB 481 GTSVITGPGTGGDILRNTFGDVSLOVNSPITQRYRLFRYASSDARVILTGAA 540
QY 541 STVGQGVSNMPLQKMEIGENLTSTRTYTDPSNPFSPFANPDIIIGISEQPLEGAGSI 600
DB 541 STVGQGVSNMPLQKMEIGENLTSTRTYTDPSNPFSPFANPDIIIGISEQPLEGAGSI 600
QY 601 SSGELYDKIEIILADATFEASDLERAQKAVNALFTSSNOIGLKTVDYDHYDQVSNLV 660
DB 601 SSGELYDKIEIILADATFEASDLERAQKAVNALFTSSNOIGLKTVDYDHYDQVSNLV 660
QY 661 DCLSDFCLEKELSEKVKHAKLSDERNLLQDPNFRGINRQPDRCGWSGTDITIQGGD 720
DB 661 DCLSDFCLEKELSEKVKHAKLSDERNLLQDPNFRGINRQPDRCGWSGTDITIQGGD 720
QY 721 DVFENYVTLPGTVDECYPTLYQKIDESKLKAYTRYELRGYIEDSDQLEIYLIRYNAKH 780
DB 721 DVFENYVTLPGTVDECYPTLYQKIDESKLKAYTRYELRGYIEDSDQLEIYLIRYNAKH 780
QY 781 EIVNVPGTGSIMPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823
DB 781 EIVNVPGTGSIMPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 10

US-09-001-982-2
; Sequence 2, Application US/09001982
; Patent No. 6204246
; GENERAL INFORMATION:
; APPLICANT: Bosch, Hendrick J.
; APPLICANT: Stiekema, Willem J.
; TITLE OF INVENTION: Hybrid Toxin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6204246artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/001,982
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/602,737
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8687
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1189 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-001-982-2
Query Match 98.4%; Score 4289; DB 3; Length 1189;
Best Local Similarity 98.9%; Pred. NO. 0;
Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 MEENNOQICPYNCLSPNEEVLIDGERISTGNSSIDISLVQFLVSNFVPGGFLVGLI 60

DB 1 MEENNOQICPYNCLSPNEEVLIDGERISTGNSSIDISLVQFLVSNFVPGGFLVGLI 60
QY 61 DFWMGIVGPSQWDAFLVQIEQLINERIAEFARNAANLANEGLGNFNFIYVEAFKEWEDP 120
DB 61 DFWMGIVGPSQWDAFLVQIEQLINERIAEFARNAANLANEGLGNFNFIYVEAFKEWEDP 120
QY 121 NNPAETRTVIDRFLDGLLERDIPFRISGFVEPLLSVYAAANLHAILLARDSVIFGER 180
DB 121 NNPAETRTVIDRFLDGLLERDIPFRISGFVEPLLSVYAAANLHAILLARDSVIFGER 180
QY 181 WGLTTNNVNNYRLIRHIDEVADHCANTYNGRNNLPKSTYQDMTITNNRLRDLTITVL 240
DB 181 WGLTTNNVNNYRLIRHIDEVADHCANTYNGRNNLPKSTYQDMTITNNRLRDLTITVL 240
QY 241 DIAAFPNYDNRPIQPVQLREVYTDPLINFNPOLQSVQALPTFNWMESSAIRPHL 300
DB 241 DIAAFPNYDNRPIQPVQLREVYTDPLINFNPOLQSVQALPTFNWMESSAIRPHL 300
QY 301 FDIILNMTITFTDWFSGVGNFWGHRVTSISLIGGNITSPITYGREANQEPRESFTFNGPV 360
DB 301 FDIILNMTITFTDWFSGVGNFWGHRVTSISLIGGNITSPITYGREANQEPRESFTFNGPV 360
QY 361 FRTLSPTLRLLQPCQRRHFNLRGGEGVEFSTPTNSFTYGRGTVDLSITELPPEDNSVP 420
DB 361 FRTLSPTLRLLQPCQRRHFNLRGGEGVEFSTPTNSFTYGRGTVDLSITELPPEDNSVP 420
QY 421 PREGYSHRLCHATFVQSRGTPFTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
DB 421 PREGYSHRLCHATFVQSRGTPFTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
QY 481 GTSVITGPGTGGDILRNTFGDVSLOVNSPITQRYRLFRYASSDARVILTGAA 540
DB 481 GTSVITGPGTGGDILRNTFGDVSLOVNSPITQRYRLFRYASSDARVILTGAA 540
QY 541 STVGQGVSNMPLQKMEIGENLTSTRTYTDPSNPFSPFANPDIIIGISEQPLEGAGSI 600
DB 541 STVGQGVSNMPLQKMEIGENLTSTRTYTDPSNPFSPFANPDIIIGISEQPLEGAGSI 600
QY 601 SSGELYDKIEIILADATFEASDLERAQKAVNALFTSSNOIGLKTVDYDHYDQVSNLV 660
DB 601 SSGELYDKIEIILADATFEASDLERAQKAVNALFTSSNOIGLKTVDYDHYDQVSNLV 660
QY 661 DCLSDFCLEKELSEKVKHAKLSDERNLLQDPNFRGINRQPDRCGWSGTDITIQGGD 720
DB 661 DCLSDFCLEKELSEKVKHAKLSDERNLLQDPNFRGINRQPDRCGWSGTDITIQGGD 720
QY 721 DVFENYVTLPGTVDECYPTLYQKIDESKLKAYTRYELRGYIEDSDQLEIYLIRYNAKH 780
DB 721 DVFENYVTLPGTVDECYPTLYQKIDESKLKAYTRYELRGYIEDSDQLEIYLIRYNAKH 780
QY 781 EIVNVPGTGSIMPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823
DB 781 EIVNVPGTGSIMPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 11

US-09-337-635-12
; Sequence 12, Application US/09337635
; Patent No. 6313378
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; Gilmer, Amy Jelen
; Mettus, Anne-Marie Light
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
; LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA

ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/337,635
FILING DATE: 21-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/980,071
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-337-635-12

Query Match 98.4%; Score 4289; DB 4; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 MEENNNQCIIPYCNLSNPEVLDGERISTGNSIDISLSVQFLVSNFVPGGFLVGLI 60
DB 1 MEENNNQCIIPYCNLSNPEVLDGERISTGNSIDISLSVQFLVSNFVPGGFLVGLI 60
QY 61 DFVWGVGPSQWDAFLVQIEQLINERIAEPARNAAIANLEGLNNTNIVYAEKWEEDP 120
DB 61 DFVWGVGPSQWDAFLVQIEQLINERIAEPARNAAIANLEGLNNTNIVYAEKWEEDP 120
QY 121 NNPATRTRVDRRIIDGLLERIDPSFRISGFEVPLLSVYQAANHLAILRDSVIFGER 180
DB 121 NNPATRTRVDRRIIDGLLERIDPSFRISGFEVPLLSVYQAANHLAILRDSVIFGER 180
QY 181 WGLTTINVENYNNLRIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRDLTLTVL 240
DB 181 WGLTTINVENYNNLRIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRDLTLTVL 240
QY 241 DIAAFPNNYDNRRIPIQPVQQLTRVYTDPLINFNPQLQSVQALPTFNWMESSAIRNPHL 300
DB 241 DIAAFPNNYDNRRIPIQPVQQLTRVYTDPLINFNPQLQSVQALPTFNWMESSAIRNPHL 300
QY 301 FDLINLLTIPTDFWFSGRNFWGCHRVISLIGGNITSPIYGREANQPPRSFTFNGPV 360
DB 301 FDLINLLTIPTDFWFSGRNFWGCHRVISLIGGNITSPIYGREANQPPRSFTFNGPV 360
QY 361 FRTLSTPTLRLLQPCQRHHNLRGEGVEFTPTNSFTYRGVTDVDSLTELPPDNSVP 420
DB 361 FRTLSTPTLRLLQPCQRHHNLRGEGVEFTPTNSFTYRGVTDVDSLTELPPDNSVP 420
QY 421 PREGYSHRLCHATFVQSGTFFLTGTVFVSWTHRSATLNTIDPERINQIPLVKGFRVWG 480
DB 421 PREGYSHRLCHATFVQSGTFFLTGTVFVSWTHRSATLNTIDPERINQIPLVKGFRVWG 480
QY 481 GTSVITGPGETGDIILRNFTFGDFVSLQNNINSPIQTRRLRPYASSRDARVIVLTGAA 540
DB 481 GTSVITGPGETGDIILRNFTFGDFVSLQNNINSPIQTRRLRPYASSRDARVIVLTGAA 540
QY 541 STGVGGQVSNMPLQKTMIEIGENLTSTRTRYTDFSNPFSFRANPDIIIGISEQPLFCAGSI 600
DB 541 STGVGGQVSNMPLQKTMIEIGENLTSTRTRYTDFSNPFSFRANPDIIIGISEQPLFCAGSI 600

QY 601 SSGELYIDKIEILLADATFEASDLERAQKAVNALFTSSNQIGLKTVDVTDYHIDQVSNLV 660
DB 601 SSGELYIDKIEILLADATFEASDLERAQKAVNALFTSSNQIGLKTVDVTDYHIDQVSNLV 660
QY 661 DCLSDPEFCLDEKRELSKVKHAKRLSDERNLQDPNFRGINRQPDGRWGSDTITIQGGD 720
DB 661 DCLSDPEFCLDEKRELSKVKHAKRLSDERNLQDPNFRGINRQPDGRWGSDTITIQGGD 720
QY 721 DVFKENYVTLPGTVDECYPTLYQKIDESKLAAYTRYELRGYIEDSQDLIEYLIRYNAKH 780
DB 721 DVFKENYVTLPGTVDECYPTLYQKIDESKLAAYTRYELRGYIEDSQDLIEYLIRYNAKH 780
QY 781 EIVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 833
DB 781 EIVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 833

RESULT 12
US-09-337-280-12
Sequence 12, Application US/09337280
Patent No. 6423828
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Gilmer, Amy Jelen
APPLICANT: Mettue, Anne-Marie Light
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
TITLE OF INVENTION: LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/337,280
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/980,071
FILING DATE:
APPLICATION NUMBER: US 08/757,536
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-337-280-12

Query Match 98.4%; Score 4289; DB 4; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 MEENNNQCIIPYCNLSNPEVLDGERISTGNSIDISLSVQFLVSNFVPGGFLVGLI 60
DB 1 MEENNNQCIIPYCNLSNPEVLDGERISTGNSIDISLSVQFLVSNFVPGGFLVGLI 60
QY 61 DFVWGVGPSQWDAFLVQIEQLINERIAEPARNAAIANLEGLNNTNIVYAEKWEEDP 120

Db 61 DFVNGVGSQWDAFLVQEQINERIAEFARNAANLEGLGNFNIVVEAFKEWEDP 120
Qy 121 NNPAIRTRVIDRFLDGLLERDIPSRISGFEVPLLSVYAQAANHLALRDSVIFGER 180
Db 121 NNPAIRTRVIDRFLDGLLERDIPSRISGFEVPLLSVYAQAANHLALRDSVIFGER 180
Qy 181 WGLTTINVENYNNLRIRHIDYADHCANTYNGLNLPKSTYQDWITYNLRDLTLVL 240
Db 181 WGLTTINVENYNNLRIRHIDYADHCANTYNGLNLPKSTYQDWITYNLRDLTLVL 240
Qy 241 DIAAFFPNYNNRRYPIQPVQGLTREVTYDPLINFPNQLSQVAQLPTFNWESSAIRNPHL 300
Db 241 DIAAFFPNYNNRRYPIQPVQGLTREVTYDPLINFPNQLSQVAQLPTFNWESSAIRNPHL 300
Qy 301 FDIILNNLTFTDWFSGVGRNFWGGRHVVISLIGGNITSPYIGREANQEPFRFTNGPV 360
Db 301 FDIILNNLTFTDWFSGVGRNFWGGRHVVISLIGGNITSPYIGREANQEPFRFTNGPV 360
Qy 361 FRTLSIPTLRLLQPCQRRHFNLRGEGVEFSTPTNSFTYGRGTVDLSLTELPPEDNSVP 420
Db 361 FRTLSIPTLRLLQPCQRRHFNLRGEGVEFSTPTNSFTYGRGTVDLSLTELPPEDNSVP 420
Qy 421 PREGYSHRLCHATFVQSGTPELTGTVVFWSTHRSATLTNTIDPERINQIPLVKGRVWG 480
Db 421 PREGYSHRLCHATFVQSGTPELTGTVVFWSTHRSATLTNTIDPERINQIPLVKGRVWG 480
Qy 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNNINSPITQRYRLFRFYASSRDARVILVTGAA 540
Db 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNNINSPITQRYRLFRFYASSRDARVILVTGAA 540
Qy 541 STGVGGQVSNMPLQKTMIEGENLTSTRFTYDPSNPPFRANPDIIIGISQPLFGAGSI 600
Db 541 STGVGGQVSNMPLQKTMIEGENLTSTRFTYDPSNPPFRANPDIIIGISQPLFGAGSI 600
Qy 601 SSGELYIDKIEILADATFEASDLERAQAVNALTSNQGILKTDVTHYHIDQVSNLV 660
Db 601 SSGELYIDKIEILADATFEASDLERAQAVNALTSNQGILKTDVTHYHIDQVSNLV 660
Qy 661 DCLSDFCDEKRELSEKVKHAKRLSDERNLLODPNFRGINQDPGRWGSTDTITQQGD 720
Db 661 DCLSDFCDEKRELSEKVKHAKRLSDERNLLODPNFRGINQDPGRWGSTDTITQQGD 720
Qy 721 DVFKENYVTLGTVDECYPTLYQKIDESKIKATRYELRGVIEDSQDLBIYLIYRNAXH 780
Db 721 DVFKENYVTLGTVDECYPTLYQKIDESKIKATRYELRGVIEDSQDLBIYLIYRNAXH 780
Qy 781 EIVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
Db 781 EIVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 13
US-07-828-788A-16
Sequence 16, Application US/07828788A
Patent No. 5273746
GENERAL INFORMATION:
APPLICANT: PAYNE, JEWEL M.
APPLICANT: HICKLE, LESLIE A.
TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID R. SALIWANCHIK
STREET: 2421 N.W. 41st STREET, SUITE A-1
CITY: GAINESVILLE
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/828,788A
FILING DATE: 19920129
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SALIWANCHIK, DAVID R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
STRAIN: AIZAWAI
INDIVIDUAL ISOLATE: PS911
IMMEDIATE SOURCE:
LIBRARY: LAMEDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
CLONE: 81B2
US-07-828-788A-16

Query Match 98.4%; Score 4288; DB 1; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 MEENNONQCIYPNCLSNPEEVLDERISTGNSSIDISLSVQPLVSNFVGGGLVGLI 60
Db 1 MEENNONQCIYPNCLSNPEEVLDERISTGNSSIDISLSVQPLVSNFVGGGLVGLI 60
Qy 61 DFVNGVGSQWDAFLVQEQINERIAEFARNAANLEGLGNFNIVVEAFKEWEDP 120
Db 61 DFVNGVGSQWDAFLVQEQINERIAEFARNAANLEGLGNFNIVVEAFKEWEDP 120
Qy 121 NNPAIRTRVIDRFLDGLLERDIPSRISGFEVPLLSVYAQAANHLALRDSVIFGER 180
Db 121 NNPAIRTRVIDRFLDGLLERDIPSRISGFEVPLLSVYAQAANHLALRDSVIFGER 180
Qy 181 WGLTTINVENYNNLRIRHIDYADHCANTYNGLNLPKSTYQDWITYNLRDLTLVL 240
Db 181 WGLTTINVENYNNLRIRHIDYADHCANTYNGLNLPKSTYQDWITYNLRDLTLVL 240
Qy 241 DIAAFFPNYNNRRYPIQPVQGLTREVTYDPLINFPNQLSQVAQLPTFNWESSAIRNPHL 300
Db 241 DIAAFFPNYNNRRYPIQPVQGLTREVTYDPLINFPNQLSQVAQLPTFNWESSAIRNPHL 300
Qy 301 FDIILNNLTFTDWFSGVGRNFWGGRHVVISLIGGNITSPYIGREANQEPFRFTNGPV 360
Db 301 FDIILNNLTFTDWFSGVGRNFWGGRHVVISLIGGNITSPYIGREANQEPFRFTNGPV 360
Qy 361 FRTLSIPTLRLLQPCQRRHFNLRGEGVEFSTPTNSFTYGRGTVDLSLTELPPEDNSVP 420
Db 361 FRTLSIPTLRLLQPCQRRHFNLRGEGVEFSTPTNSFTYGRGTVDLSLTELPPEDNSVP 420
Qy 421 PREGYSHRLCHATFVQSGTPELTGTVVFWSTHRSATLTNTIDPERINQIPLVKGRVWG 480
Db 421 PREGYSHRLCHATFVQSGTPELTGTVVFWSTHRSATLTNTIDPERINQIPLVKGRVWG 480
Qy 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNNINSPITQRYRLFRFYASSRDARVILVTGAA 540
Db 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNNINSPITQRYRLFRFYASSRDARVILVTGAA 540
Qy 541 STGVGGQVSNMPLQKTMIEGENLTSTRFTYDPSNPPFRANPDIIIGISQPLFGAGSI 600
Db 541 STGVGGQVSNMPLQKTMIEGENLTSTRFTYDPSNPPFRANPDIIIGISQPLFGAGSI 600

QY 601 SSGELYIDKIEIILADATFAESDLERAQKAVNALFTSSNOIGLTKTDTVDYHIDQVSNLV 660
DB 601 SSGELYIDKIEIILADATFAESDLERAQKAVNALFTSSNOIGLTKTDTVDYHIDQVSNLV 660
QY 661 DCLSDPCLDEKRELSKVHAKLSDERNLQDPNFRGINRQPDGRGWRGSTDITIQGGD 720
DB 661 DCLSDPCLDEKRELSKVHAKLSDERNLQDPNFRGINRQPDGRGWRGSTDITIQGGD 720
QY 721 DVFKNYVTLPGTVDECPYLYQKIDESKLKAYTRYELRGYIEDSQDLBIYLIYNAKH 780
DB 721 DVFKNYVTLPGTVDECPYLYQKIDESKLKAYTRYELRGYIEDSQDLBIYLIYNAKH 780
QY 781 EIVNVPGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823
DB 781 EIVNVPGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 14

US-08-356-034-6
; Sequence 6, Application US/08356034
; Patent No. 5691308
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Sick, August J.
; TITLE OF INVENTION: No. 5691308el Bacillus thuringiensis Isolate
; TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding
; TITLE OF INVENTION: No. 5691308el Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,034
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/210,110
; FILING DATE:
; APPLICATION NUMBER: 07/865,168
; FILING DATE: 09-APR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/451,261
; FILING DATE: 14-DEC-89
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/371,955
; FILING DATE: 27-JUN-89
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, Roman
; REGISTRATION NUMBER: 21,023
; REFERENCE/DOCKET NUMBER: MA43.C1.D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904)375-8100
; TELEFAX: (904)372-5800
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1189 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES

; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: BACILLUS THURINGIENSIS
; STRAIN: AIZAWAI
; INDIVIDUAL ISOLATE: PS811
; IMMEDIATE SOURCE:
; LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
; CLONE: 811B2
; US-08-356-034-6

Query Match 98.4%; Score 4288; DB 1; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 MEENNQNCIPYNCLSNPEVLLDGERISTGSSSIDISLSLVQFLVSNFVPGGFLVGLI 60
DB 1 MEENNQNCIPYNCLSNPEVLLDGERISTGSSSIDISLSLVQFLVSNFVPGGFLVGLI 60
QY 61 DFVWGVGPSQWDAFLVQIEQLINERIAAFARNAAIANLEGLNNTNFIYVEAFKEWEDP 120
DB 61 DFVWGVGPSQWDAFLVQIEQLINERIAAFARNAAIANLEGLNNTNFIYVEAFKEWEDP 120
QY 121 NNPATRVIDRPRILDGLLERRDIPSFRISSGFEVPLLSUYAQAANLHLAIRDSVIFGR 180
DB 121 NNPATRVIDRPRILDGLLERRDIPSFRISSGFEVPLLSUYAQAANLHLAIRDSVIFGR 180
QY 181 WGLTTINNVNENYRLIRHIDEVADHCANTYNNGLNLPKSTYQDMWITYNRLRDLTLTVL 240
DB 181 WGLTTINNVNENYRLIRHIDEVADHCANTYNNGLNLPKSTYQDMWITYNRLRDLTLTVL 240
QY 241 DIAAPFPNDNRRYPIQPVQQLTREVTPLINFPNQLQSVQALPTFNWESSAIRNPHL 300
DB 241 DIAAPFPNDNRRYPIQPVQQLTREVTPLINFPNQLQSVQALPTFNWESSAIRNPHL 300
QY 301 FDLANLTIPTDWFSGVRNFGYGGHVRVSSLLGGGNTSPYVCREANQPPRSFTNGPV 360
DB 301 FDLANLTIPTDWFSGVRNFGYGGHVRVSSLLGGGNTSPYVCREANQPPRSFTNGPV 360
QY 361 FRTLSPITLRLQOQCORHFNLRGEGVEFSTPTNSFTYRGRTVDSTLTLPDENSV 420
DB 361 FRTLSPITLRLQOQCORHFNLRGEGVEFSTPTNSFTYRGRTVDSTLTLPDENSV 420
QY 421 PREGYSHRLCHATFVQSGTPELTGGVFWFSWTHRSATLNTIDPERINQIPLVKGFRV 480
DB 421 PREGYSHRLCHATFVQSGTPELTGGVFWFSWTHRSATLNTIDPERINQIPLVKGFRV 480
QY 481 GTSVITGPGTGGDILRRNTFGDVSQVNSPITQRYLRFRYASSRDARVILTGAA 540
DB 481 GTSVITGPGTGGDILRRNTFGDVSQVNSPITQRYLRFRYASSRDARVILTGAA 540
QY 541 STGVGGQVSVNMPLOKTMIEIGENLTSRTPRYTDFSNPFSFRANPDIIGISEQPLFCAGSI 600
DB 541 STGVGGQVSVNMPLOKTMIEIGENLTSRTPRYTDFSNPFSFRANPDIIGISEQPLFCAGSI 600
QY 601 SSGELYIDKIEIILADATFAESDLERAQKAVNALFTSSNOIGLTKTDTVDYHIDQVSNLV 660
DB 601 SSGELYIDKIEIILADATFAESDLERAQKAVNALFTSSNOIGLTKTDTVDYHIDQVSNLV 660
QY 661 DCLSDPCLDEKRELSKVHAKLSDERNLQDPNFRGINRQPDGRGWRGSTDITIQGGD 720
DB 661 DCLSDPCLDEKRELSKVHAKLSDERNLQDPNFRGINRQPDGRGWRGSTDITIQGGD 720
QY 721 DVFKNYVTLPGTVDECPYLYQKIDESKLKAYTRYELRGYIEDSQDLBIYLIYNAKH 780
DB 721 DVFKNYVTLPGTVDECPYLYQKIDESKLKAYTRYELRGYIEDSQDLBIYLIYNAKH 780
QY 781 EIVNVPGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823
DB 781 EIVNVPGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 15
US-08-980-071-2

Sequence 2, Application US/08980071
Patent No. 5914318
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Gilmer, Anne Marie Light
APPLICANT: Mettue, Anne Marie Light
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/980,071
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/757,536
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-980-071-2

Query Match 98.4%; Score 4288; DB 2; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 MEENNQCIPYCLNPNPEVLLDGERISTGNSIDISLSVQLVSNFVPGGFLVGLI 60
DB 1 MEENNQCIPYCLNPNPEVLLDGERISTGNSIDISLSVQLVSNFVPGGFLVGLI 60
QY 61 DFVWGI VGPSQWDAFLVQIEQLINERIAEFARNAANLEGLGNPNFIYVEAFKEWEEDP 120
DB 61 DFVWGI VGPSQWDAFLVQIEQLINERIAEFARNAANLEGLGNPNFIYVEAFKEWEEDP 120
QY 121 NNPA TRTRVIDRPRILDLGLLDRIDPSRISGFVEPLLSVYQAANLHLAIRDSVIFGER 180
DB 121 NNPA TRTRVIDRPRILDLGLLDRIDPSRISGFVEPLLSVYQAANLHLAIRDSVIFGER 180
QY 181 WGLTTINNVNENYELRHIDEVADHCANTYNGNINLPKSTYQDWITYNRLRDLTLTVL 240
DB 181 WGLTTINNVNENYELRHIDEVADHCANTYNGNINLPKSTYQDWITYNRLRDLTLTVL 240
QY 241 DTAARFNNRYPIQPVQGLTREVYTDPLINPOLQSVQLPTFNWESSAIRNPHL 300
DB 241 DTAARFNNRYPIQPVQGLTREVYTDPLINPOLQSVQLPTFNWESSAIRNPHL 300
QY 301 FDLNLANLIFTDWFSGVGRNFGYGHVVISLIGGNITSPYIGREANQEPGRFTNGPV 360
DB 301 FDLNLANLIFTDWFSGVGRNFGYGHVVISLIGGNITSPYIGREANQEPGRFTNGPV 360
QY 361 FRTLSIPTLRLLQOPCORHHFNLRGEVGFSTPTNSFTYRGKTVDSLTLPEDNSVP 420

Db 361 FRTLSIPTLRLLQOPCORHHFNLRGEVGFSTPTNSFTYRGKTVDSLTLPEDNSVP 420
QY 421 PREGYSHRLCHATFVQSRGTPFLTGTGVFWSWTHRSATLTNTIDPERINQIPLVKGRVWG 480
Db 421 PREGYSHRLCHATFVQSRGTPFLTGTGVFWSWTHRSATLTNTIDPERINQIPLVKGRVWG 480
QY 481 GTSVITGPGFTGGDILRENTFGDFVSLQVNSPITQRYLRFRYASSRDARVIVLTGAA 540
Db 481 GTSVITGPGFTGGDILRENTFGDFVSLQVNSPITQRYLRFRYASSRDARVIVLTGAA 540
QY 541 STGVGGOVSNMPLQKMEIGENLTSTRTFRTDFSNPFSFRANPDIIIGISEQLFAGAGSI 600
Db 541 STGVGGOVSNMPLQKMEIGENLTSTRTFRTDFSNPFSFRANPDIIIGISEQLFAGAGSI 600
QY 601 SSGELYDKIEIILADATFEASDLERAQKANNALFTSSNOIGLKTDTVDYHIDQVSNLV 660
Db 601 SSGELYDKIEIILADATFEASDLERAQKANNALFTSSNOIGLKTDTVDYHIDQVSNLV 660
QY 661 DCLSEDFCLDEKRELSEKVKHAKLSDERNLLQDNFRGINRQDRGWSGTDITIQGD 720
Db 661 DCLSEDFCLDEKRELSEKVKHAKLSDERNLLQDNFRGINRQDRGWSGTDITIQGD 720
QY 721 DVFKENYVTLPGTVDECYPTYLYOKIDESKLYKAYTRYELRGYIIESQDLLEYLIYLNAXH 780
Db 721 DVFKENYVTLPGTVDECYPTYLYOKIDESKLYKAYTRYELRGYIIESQDLLEYLIYLNAXH 780
QY 781 EIVNVPGTGSLMPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
Db 781 EIVNVPGTGSLMPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

Search completed: October 9, 2003, 13:27:36
Job time : 36 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 13:11:09 ; Search time 86 Seconds
(without alignments)
1518.976 Million cell updates/sec

Title: US-09-918-485-2
Perfect score: 4358
Sequence: 1 MEENNOQIPYNCLNPEE.....GEPNRCAPHLEWNPDLDCSC 823

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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3:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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21:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4348	99.8	823	9 AAP80972	Sequence encoded b
2	4339	99.6	823	9 AAP81502	delta-endotoxin ag
3	4294	98.5	1189	12 AAR10130	Lepidopteran-activ
4	4289	98.4	1189	12 AAR10193	Insecticidal cryst
5	4289	98.4	1189	16 AAR71463	Crystall protein en
6	4289	98.4	1189	19 AAW61340	A mutated CryIC pr
7	4289	98.4	1189	20 AAY17793	B. thuringiensis c
8	4289	98.4	1189	21 AAY82401	Bacillus thuringie
9	4289	98.4	1189	23 AAE26465	Bacillus thuringie

10	4289	98.4	1189	23 ABG93819	B. thuringiensis C
11	4288	98.4	1189	14 AAR39757	Delta endotoxin.
12	4288	98.4	1189	19 AAW61337	A mutated CryIC pr
13	4288	98.4	1189	19 AAW61335	A mutated CryIC pr
14	4288	98.4	1189	20 AAY17790	B. thuringiensis c
15	4288	98.4	1189	20 AAY17788	B. thuringiensis c
16	4288	98.4	1189	21 AAY82398	Bacillus thuringie
17	4288	98.4	1189	21 AAY82398	Bacillus thuringie
18	4288	98.4	1189	23 AAE26460	Bacillus thuringie
19	4288	98.4	1189	23 AAE26462	Bacillus thuringie
20	4288	98.4	1189	23 ABG93814	B. thuringiensis C
21	4288	98.4	1189	23 ABG93816	B. thuringiensis C
22	4287	98.4	1189	19 AAW61336	A mutated CryIC pr
23	4287	98.4	1189	20 AAY17789	B. thuringiensis c
24	4287	98.4	1189	21 AAY82397	Bacillus thuringie
25	4287	98.4	1189	23 AAE26461	Bacillus thuringie
26	4287	98.4	1189	23 ABG93815	B. thuringiensis C
27	4283	98.3	1189	19 AAW61339	A mutated CryIC pr
28	4283	98.3	1189	20 AAY17792	B. thuringiensis c
29	4283	98.3	1189	23 AAE26464	Bacillus thuringie
30	4283	98.3	1189	23 AAE26464	Bacillus thuringie
31	4283	98.3	1189	23 ABG93818	B. thuringiensis C
32	4282	98.3	1189	19 AAW61338	A mutated CryIC pr
33	4282	98.3	1189	19 AAW61345	a mutated CryIC pr
34	4282	98.3	1189	20 AAY17791	B. thuringiensis c
35	4282	98.3	1189	20 AAY17783	EG12111 crystal pr
36	4282	98.3	1189	21 AAY82399	Bacillus thuringie
37	4282	98.3	1189	21 AAY82431	Bacillus thuringie
38	4282	98.3	1189	23 AAE26463	Bacillus thuringie
39	4282	98.3	1189	23 AAE26471	Bacillus thuringie
40	4282	98.3	1189	23 ABG93817	B. thuringiensis C
41	4282	98.3	1189	23 ABG93849	B. thuringiensis C
42	4281	98.2	1189	19 AAW61346	A mutated CryIC pr
43	4281	98.2	1189	20 AAY17784	EG12121 crystal pr
44	4281	98.2	1189	21 AAY82432	Bacillus thuringie
45	4281	98.2	1189	23 AAE26472	Bacillus thuringie

ALIGNMENTS

RESULT 1
AAP80972
ID AAP80972 standard; protein; 823 AA.
XX
AC AAP80972;
XX
DT 25-MAR-2003 (updated)
DT 30-OCT-1990 (first entry)
XX
DE Sequence encoded by 3kb Hind III-Pst I fragment of Bacillus
DE thuringiensis (BT) strain aizawai 7-29 and entomocidus 6-01.
XX
KW Microbial insecticide; pesticide; bacterium; Noctuellae;
KW Spodoptera littoralis; Mammestra brassicae.
OS Bacillus thuringiensis.
XX
PN EP295156-A.
XX
PD 14-DEC-1988.
XX
PF 06-MAY-1988; 88EP-0401121.
XX
PR 10-JUN-1987; 87FR-0008090.
XX
(INSP) INST PASTEUR.
PA (CNRS) CENT NAT RECH SCI.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
XX
PI Sanchis V, Lereclus D, Menou G, Lecadet MM, Martouret D, Dedonder R;
XX WPI; 1988-355565/50.
DR

XX New DNA sequences encoding insecticidal polypeptide -
PT with specific activity against lepidoptera larvae esp.
PT Spodoptera littoralis
XX
XX Claim 14; Pages 27-29; 37pp; French.
XX
XX It is at least part of the N-terminal region of a polypeptide which is
CC specifically toxic for lepidopteran larvae of the family Noctuidae
CC (esp. Spodoptera littoralis). The DNA encoding it can be incorporated
CC directly in plants or micro-organisms, pref. Pseudomonas, Azospirillum
CC or Rhizobium, which live in the plant environment.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 823 AA;
SQ Query Match 99.8%; Score 4348; DB 9; Length 823;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 822; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MEENNQCIPYNCLSNPEVLLDGERISTGSSIDISLSVQLVSNFVPGGFLVGLI 60
Db 1 MEENNQCIPYNCLSNPEVLLDGERISTGSSIDISLSVQLVSNFVPGGFLVGLI 60
Qy 61 DFVWGIQVPSQWDAFLVQIQLINERIAEFARNAANLEGLGNFNIVYVEAFKEWEDP 120
Db 61 DFVWGIQVPSQWDAFLVQIQLINERIAEFARNAANLEGLGNFNIVYVEAFKEWEDP 120
Qy 121 NNPATRTRVIDRFRILDLGLERDIPSPRISGFVPLLSVYQAANLHLAIRDVSIFGER 180
Db 121 NNPATRTRVIDRFRILDLGLERDIPSPRISGFVPLLSVYQAANLHLAIRDVSIFGER 180
Qy 181 WGLTINVENNRLRHIDEVADHCANTYNGLNLPKSTYQDWITYNRLRDLTLVL 240
Db 181 WGLTINVENNRLRHIDEVADHCANTYNGLNLPKSTYQDWITYNRLRDLTLVL 240
Qy 241 DTAAEPFNDRYPTOPVQOLITREVYTDPLINPQLOSLVAQLPTFNWESSAINEPHL 300
Db 241 DTAAEPFNDRYPTOPVQOLITREVYTDPLINPQLOSLVAQLPTFNWESSAINEPHL 300
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Db 301 FOILNNLTFTDFSVGRNPFYWGHRVYSSLIQGNITSPYGRANQEPFRFTNGEV 360
Qy 361 FRTLSIPTLRLLQPCORHFNLRGEGVEFSTPNSFTYRGRGTVDLSLTLPEDNSVP 420
Db 361 FRTLSIPTLRLLQPCORHFNLRGEGVEFSTPNSFTYRGRGTVDLSLTLPEDNSVP 420
Qy 421 PREGYSHRLCHATPVQSGTPTLTGTVFVSWTHRSATLNTIDPERINQIPLVKGFRVWG 480
Db 421 PREGYSHRLCHATPVQSGTPTLTGTVFVSWTHRSATLNTIDPERINQIPLVKGFRVWG 480
Qy 481 GTSVITGPGTGGDILRRNTFGDVSQVNSINSPITQRYRLFRFYASSRDARVILTGAA 540
Db 481 GTSVITGPGTGGDILRRNTFGDVSQVNSINSPITQRYRLFRFYASSRDARVILTGAA 540
Qy 541 STGVGQGVSNMPLQKTMEIGENLTSRFTYDPSNPFSPFRANPDIIIGISQPLFAGSI 600
Db 541 STGVGQGVSNMPLQKTMEIGENLTSRFTYDPSNPFSPFRANPDIIIGISQPLFAGSI 600
Qy 601 SGEYVYDKIEIILADATFEASDLERAKAVNALFTSSNOIGLKTVDYHIDQVSNLV 660
Db 601 SGEYVYDKIEIILADATFEASDLERAKAVNALFTSSNOIGLKTVDYHIDQVSNLV 660
Qy 661 DCLSEBFLDEKRELSEKVKAKLSDEENLLODPNFRGNQPPDRGWRGSDTITQGGD 720
Db 661 DCLSEBFLDEKRELSEKVKAKLSDEENLLODPNFRGNQPPDRGWRGSDTITQGGD 720
Qy 721 DVFKNYTLGCTVDECPYLYOKIDESKLYKATRYELRGVIEDSOLEYLYIAYNAKH 780
Db 721 DVFKNYTLGCTVDECPYLYOKIDESKLYKATRYELRGVIEDSOLEYLYIAYNAKH 780
Qy 781 EIVNVPGTGSMLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

Db 781 EIVNVPGTGSMLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
RESULT 2
AAP81502
ID AAP81502 standard; protein; 823 AA.
XX
XX AAP81502;
AC
XX 25-MAR-2003 (updated)
DT 23-OCT-1990 (first entry)
XX
XX delta-endotoxin against Lepidoptera larvae.
DB
XX Lepidoptera larvae; insecticide; Bacillus thuringiensis;
KW Spodoptera littoralis; delta endotoxin; 88.
XX
XX synthetic.
OS
XX Key Location/Qualifiers
FH 1..620
FT Region
FT /label=N-terminal half
FT /note="responsible for toxicity"
XX
XX WO8809812-A.
XX
XX 15-DEC-1988.
PD
XX 09-JUN-1988; 88WO-FR00292.
XX
XX 10-JUN-1987; 87FR-0008090.
PR
XX 06-MAY-1988; 88EP-0401121.
PR
XX (INSP) INST PASTEUR.
PA (INSP) INST NAT RECH AGRONOMIQ.
PA
XX Sanchis V, Lereclus D, Menou G;
XX
XX WPI; 1988-368627/51.
XX
XX N-PSDB; AAN81949.
XX
XX New nucleotide sequences encoding new polypeptide -
PT with selective action against lepidopteran larvae esp Spodoptera
FT littoralis
XX
XX Claim 14; Page 52; 65pp; French.
PS
XX Polypeptide is encoded by a 3kb HindIII-PstI fragment of
CC Bacillus thuringiensis. Recombinant sequences can also be
CC constructed from 2 diff strains of B.thuringiensis. The sequence
CC between bases 50 to 985 is claimed separately as this encodes "at
CC least a part of the N-terminal region of an insecticidal
CC polypeptide". There is a variable amino acid at posn 124 which is
CC Ala in the sequence given here but which is Glu in the shorter
CC sequence.
CC (Updated on 25-MAR-2003 to correct PR field.)
CC (Updated on 25-MAR-2003 to correct PA field.)
CC (Updated on 25-MAR-2003 to correct DR field.)
XX
XX Sequence 823 AA;
SQ Query Match 99.6%; Score 4339; DB 9; Length 823;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 820; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MEENNQCIPYNCLSNPEVLLDGERISTGSSIDISLSVQLVSNFVPGGFLVGLI 60
Db 1 MEENNQCIPYNCLSNPEVLLDGERISTGSSIDISLSVQLVSNFVPGGFLVGLI 60
Qy 61 DFVWGIQVPSQWDAFLVQIQLINERIAEFARNAANLEGLGNFNIVYVEAFKEWEDP 120
Db 61 DFVWGIQVPSQWDAFLVQIQLINERIAEFARNAANLEGLGNFNIVYVEAFKEWEDP 120

QY 121 NNPATRTRVIDRFRILDLGLLDRDIPSPRISGFEVPLLSVYAAQANLHLAILRDSVIFGER 180
 DB 121 NNPATRTRVIDRFRILDLGLLDRDIPSPRISGFEVPLLSVYAAQANLHLAILRDSVIFGER 180
 QY 181 WGLTTINVENNRLRHHIDEYADHCANTYNGLNLPKSTYQDWITTYNRLRDLTLTVL 240
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 DB 241 DIAAFFPNYDNRYPQIPVGQLTRVYTDPLINFNPQLQSVQALPTFNVMSSAIRNPHL 300
 QY 301 FDLINLTIPTDWFSGVGRNFWGHRVVISLIGGNITSPYIGREANQBPSPFTFNGPV 360
 DB 301 FDLINLTIPTDWFSGVGRNFWGHRVVISLIGGNITSPYIGREANQBPSPFTFNGPV 360
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 DB 421 PREGYSHRLCHATFVQSGTPTPLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
 QY 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNINSPIQRYRLRPRYASSRDARVIVLTGAA 540
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 QY 541 STVGGOVSVNMPLOKTMETIGENLTSTRTRYTDSPNPFSPFRANPDIIGISEQPLFCAGSI 600
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 DB 661 DCLSDFCCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGSGTDITIQGSD 720
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 DB 721 DVPKENYVTLPGTVDECPYLYOKIDESKDKAYTRYELRGYIEDSDLEIYLIAYNAXH 780
 QY 781 EIVNVPETGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
 DB 781 EIVNVPETGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 3

AA10130
 ID AA10130 standard; Protein; 1189 AA.

XX AA10130;

AC 25-MAR-2003 (updated)

DT 20-MAR-1991 (first entry)

XX Lepidopteran-active toxin C.

XX Lepidopteran-active toxin C; pest control.

XX Bacillus thuringiensis PS81L (NRRL B-18484).

XX EP405810-A.

XX 02-JAN-1991.

XX 18-JUN-1990; 90EP-0306594.

XX 14-DEC-1989; 89US-0451261.

PR 27-JUN-1989; 89US-0371955.

XX (MYCO) MYCOGEN CORP.
 PA Payne J, Sick AJ;
 XX WPI; 1991-009132/02.
 DR N-PSDB; AAQ10181.
 DR
 XX Bacillus thuringiensis contg. DNA encoding lepidopteran-active
 PT toxin - use of microorganisms transformed with the toxin gene
 PT in pest control
 XX Claim 5; Page 19-23; 28pp; English.
 XX Expression of the toxin gene by a host results, directly or
 CC indirectly, in the intracellular prodn. and maintenance of the
 CC pesticide
 CC See also AAQ10179-82.
 CC (updated on 25-MAR-2003 to correct PA field.)
 XX Sequence 1189 AA;

Query Match 98.5%; Score 4294; DB 12; Length 1189;
 Best Local Similarity 99.0%; Pred. No. 0;
 Matches 815; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MEENNQNCIPYNCLSNPEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
 DB 1 MEENNQNCIPYNCLSNPEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
 QY 61 DFWMGVGSQWDAFLVQIEQLINERIAAFARNAAIANLEGIGNNFNIYVEAFKEWEEP 120
 DB 61 DFWMGVGSQWDAFLVQIEQLINERIAAFARNAAIANLEGIGNNFNIYVEAFKEWEEP 120
 QY 121 NNPATRTRVIDRFRILDLGLLDRDIPSPRISGFEVPLLSVYAAQANLHLAILRDSVIFGER 180
 DB 121 NNPATRTRVIDRFRILDLGLLDRDIPSPRISGFEVPLLSVYAAQANLHLAILRDSVIFGER 180
 QY 181 WGLTTINVENNRLRHHIDEYADHCANTYNGLNLPKSTYQDWITTYNRLRDLTLTVL 240
 DB 181 WGLTTINVENNRLRHHIDEYADHCANTYNGLNLPKSTYQDWITTYNRLRDLTLTVL 240
 QY 241 DIAAFFPNYDNRYPQIPVGQLTRVYTDPLINFNPQLQSVQALPTFNVMSSAIRNPHL 300
 DB 241 DIAAFFPNYDNRYPQIPVGQLTRVYTDPLINFNPQLQSVQALPTFNVMSSAIRNPHL 300
 QY 301 FDLINLTIPTDWFSGVGRNFWGHRVVISLIGGNITSPYIGREANQBPSPFTFNGPV 360
 DB 301 FDLINLTIPTDWFSGVGRNFWGHRVVISLIGGNITSPYIGREANQBPSPFTFNGPV 360
 QY 361 FRTLSPITLRLLOQPCORHHFNLRGGEGVEFSTPTNSFTYGRGTVDLSLTELPEPNSVP 420
 DB 361 FRTLSPITLRLLOQPCORHHFNLRGGEGVEFSTPTNSFTYGRGTVDLSLTELPEPNSVP 420
 QY 421 PREGYSHRLCHATFVQSGTPTPLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
 DB 421 PREGYSHRLCHATFVQSGTPTPLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
 QY 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNINSPIQRYRLRPRYASSRDARVIVLTGAA 540
 DB 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNINSPIQRYRLRPRYASSRDARVIVLTGAA 540
 QY 541 STVGGOVSVNMPLOKTMETIGENLTSTRTRYTDSPNPFSPFRANPDIIGISEQPLFCAGSI 600
 DB 541 STVGGOVSVNMPLOKTMETIGENLTSTRTRYTDSPNPFSPFRANPDIIGISEQPLFCAGSI 600
 QY 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLKTVDYDHDQVSNLV 660
 DB 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLKTVDYDHDQVSNLV 660
 QY 661 DCLSDFCCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGSGTDITIQGSD 720
 DB 661 DCLSDFCCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGSGTDITIQGSD 720

QY	721	DVFKENYVTLPGTVDECYPTLYQKIDESKAYTRYELGYIEDSQDLLEIYLIYNAKH	780
Db	721	DVFKENYVTLPGTVDECYPTLYQKIDESKAYTRYELGYIEDSQDLLEIYLIYNAKH	780
QY	781	EIVNVPGTSLWPLSAQSPICKGCEPNRCAPHLEWNPDLDCSC	823
Db	781	EIVNVPGTSLWPLSAQSPICKGCEPNRCAPHLEWNPDLDCSC	823
RESULT 4			
AA	10193	standard; Protein; 1189 AA.	
AC	AA10193;		
DT	25-MAR-2003	(updated)	
DT	27-MAR-1991	(first entry)	
XX	Insecticidal crystal protein (ICP) entomocidus HD-110 of gene br4.		
XX	Insecticide; Lepidoptera; Coleoptera.		
XX	Bacillus thuringiensis.		
XX	EP408403-A.		
XX	16-JAN-1991.		
XX	29-MAY-1990;	90EP-0401427.	
XX	29-MAY-1990;	90EP-0401427.	
XX	31-MAY-1989;	89EP-0401499.	
PA	(PLBZ) PLANT GENETICS SYSTEMS NV..		
PI	Vanmellaer H, Botterman J, Vanrie J, Joos H;		
DR	WPI; 1991-016587/03.		
DR	N-PSDB; AAQ10229.		
XX	Insect-resistant transgenic plant cells - transformed with genes		
PI	encoding different non-competitively binding Bacillus		
PI	thuringiensis insecticidal proteins		
XX	Disclosure; Fig 14; 82pp; English.		
PS	Sequence encoding the protein may be used in transformation of crop		
CC	plants, providing resistance to insect (esp. lepidoptera and coleoptera)		
CC	attack, without resort to insecticides which incur problems with		
CC	development of insect resistance.		
CC	(Updated on 25-MAR-2003 to correct PA field.)		
CC	(Updated on 25-MAR-2003 to correct PI field.)		
XX	Sequence 1189 AA;		
Query Match			
Best Local Similarity 98.4%; Score 4289; DB 12; Length 1189;			
Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;			
QY	1	MEENNQCIPYCNCLSNPEVLLDGERISTGNSIDISLSVQFLVSNFVPGGFLVGLI	60
Db	1	MEENNQCIPYCNCLSNPEVLLDGERISTGNSIDISLSVQFLVSNFVPGGFLVGLI	60
QY	61	DFWGIQVPSQWDAFLVOIEQLINERIAEFARNAANLEGLGNFNFIYVEAFKEWEDP	120
Db	61	DFWGIQVPSQWDAFLVOIEQLINERIAEFARNAANLEGLGNFNFIYVEAFKEWEDP	120
QY	121	NNPATRTRVIDRFRILDLGLERDIPSPRISGFVEPLLSVVAQANLHAILRDSVIFGER	180
Db	121	NNPATRTRVIDRFRILDLGLERDIPSPRISGFVEPLLSVVAQANLHAILRDSVIFGER	180
QY	181	WGTTTNNVNNYELIRHIDEYADHCANTYNGLNLPKSTYQDMITYNLRDLTLTVL	240

Db 61 DFVWGVGSQWDAFLVQIQLINERIAEFARNAALANLEGLGNFNFIYVEAFKEWEDP 120
Qy 121 NNPATRVDRFRILDLGLLDRIPSPRISGFEVPLLSVYAAQANLHAILRDSVIFGER 180
Db 121 HNPATRVDRFRILDLGLLDRIPSPRISGFEVPLLSVYAAQANLHAILRDSVIFGER 180
Qy 181 WGLTTINVENYNNRLIRHIDEYADHCANTYNNRGLNLPKSTYQDWITYNRLRDLTLTVL 240
Db 181 WGLTTINVENYNNRLIRHIDEYADHCANTYNNRGLNLPKSTYQDWITYNRLRDLTLTVL 240
Qy 241 DIAAFFPNYNNRYPQIPVQGLTREVTYDPLINFNPOLSVAQLPTFNWESSAIRNPHL 300
Db 241 DIAAFFPNYNNRYPQIPVQGLTREVTYDPLINFNPOLSVAQLPTFNWESSAIRNPHL 300
Qy 301 FDILNNLTFTDWFVSGRNFWGGRHVVISLIGGNNITSPYIGREANQBPSPRFTNGVP 360
Db 301 FDILNNLTFTDWFVSGRNFWGGRHVVISLIGGNNITSPYIGREANQBPSPRFTNGVP 360
Qy 361 FRTLSTPLRLLQOPCORHFNHNLGEGVEFTPTNSFTYGRGRTVDSLTLPEDNSVP 420
Db 361 FRTLSTPLRLLQOPWPAPPFNLRGVEGVEFTPTNSFTYGRGRTVDSLTLPEDNSVP 420
Qy 421 PREGYSRHLCHATFVQSGTPELTTGVVFSWTHRSATLNTIDPERINQIPLVKGRVWG 480
Db 421 PREGYSRHLCHATFVQSGTPELTTGVVFSWTHRSATLNTIDPERINQIPLVKGRVWG 480
Qy 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNIINSPIQRYRLFRVYASSRDARVILTGAA 540
Db 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNIINSPIQRYRLFRVYASSRDARVILTGAA 540
Qy 541 STGVGGQVNVNPLQKTMIEIGENLTSTRTFYTFDPSFPFRANPDIIIGISEQPLGAS 600
Db 541 STGVGGQVNVNPLQKTMIEIGENLTSTRTFYTFDPSFPFRANPDIIIGISEQPLGAS 600
Qy 601 SSGELYIDKIEILADATFEASDLERAKAVNALFTSSNQIGLKTDTYHIDQVSNLV 660
Db 601 SSGELYIDKIEILADATFEASDLERAKAVNALFTSSNQIGLKTDTYHIDQVSNLV 660
Qy 661 DCLSDFECLDEKRELSEKVKHAKRLSDERNLLODPNFRGQNRGWRGSDTITIQGSD 720
Db 661 DCLSDFECLDEKRELSEKVKHAKRLSDERNLLODPNFRGQNRGWRGSDTITIQGSD 720
Qy 721 DVFKENYVTLGTVDECYPTLYQKIDESKLKAYTRYELRGYIEDSQDLBIYLIYNAKH 780
Db 721 DVFKENYVTLGTVDECYPTLYQKIDESKLKAYTRYELRGYIEDSQDLBIYLIYNAKH 780
Qy 781 EIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
Db 781 EIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 7

AA117793
ID AA117793 standard; Protein; 1189 AA.
XX AC AA117793;
XX DT 12-AUG-1999 (first entry)
XX DE B. thuringiensis crystal protein CryIC.499 protein sequence.
XX KW Bacillus thuringiensis; delta-endotoxin; insecticide; crystal protein;
KW lepidopteran insect; CryIC; genetic engineering; mucagenesis; mutant;
KW caterpillar; beetle; mosquito; toxic; modification.
XX OS Bacillus thuringiensis.
OS Synthetic.
XX US5914318-A.
XX PD 22-JUN-1999.
XX PF 26-NOV-1997; 97US-0980071.

XX 26-NOV-1997; 97US-0980071.
PR 27-NOV-1996; 96US-0757536.
XX (ECOG-) ECOGEN INC.
XX Baum JA, Gilmer AJ, Mettuss AL;
XX WPI: 1999-370510/31.
DR N-PSDB; AAX80039.
XX New modified delta-endotoxin crystal proteins from Bacillus
PT thuringiensis are useful in insecticidal compositions
XX Example 13; Column 94-97; 144pp; English.
XX The present invention describes a new composition comprising an isolated
CC polypeptide for modified Bacillus thuringiensis crystal proteins (CryIC).
CC The polypeptide of the composition is insecticidally-active against
CC Lepidoptera. The composition is toxic to an insect cell and comprised
CC within an insecticidal formulation can be used as a plant protective
CC spray which is toxic to caterpillars, beetles and mosquitoes. The
CC polypeptide of the composition may be used to kill an insect through
CC ingestion of the composition directly or by ingestion of a plant coated
CC with the composition or a transgenic plant that expresses the polypeptide
CC composition. The insecticidal proteins produced by B. thuringiensis are
CC harmless to plants and other non-targeted organisms but toxic to their
CC specific target insect. The polypeptides have improved toxicity so a
CC reduced amount of bioinsecticide per unit area of treated crop can be
CC used allowing economic and efficient utilization in the field. The
CC present sequence represents a modified B. thuringiensis crystal protein.
XX Sequence 1189 AA;
SQ

Query Match 98.4%; Score 4289; DB 20; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
Qy 1 MEENNONCIPYNCNLSNPEEVLGDERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
Db 1 MEENNONCIPYNCNLSNPEEVLGDERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
Qy 61 DFVWGVGSQWDAFLVQIQLINERIAEFARNAALANLEGLGNFNFIYVEAFKEWEDP 120
Db 61 DFVWGVGSQWDAFLVQIQLINERIAEFARNAALANLEGLGNFNFIYVEAFKEWEDP 120
Qy 121 NNPATRVDRFRILDLGLLDRIPSPRISGFEVPLLSVYAAQANLHAILRDSVIFGER 180
Db 121 NNPATRVDRFRILDLGLLDRIPSPRISGFEVPLLSVYAAQANLHAILRDSVIFGER 180
Qy 181 WGLTTINVENYNNRLIRHIDEYADHCANTYNNRGLNLPKSTYQDWITYNRLRDLTLTVL 240
Db 181 WGLTTINVENYNNRLIRHIDEYADHCANTYNNRGLNLPKSTYQDWITYNRLRDLTLTVL 240
Qy 241 DIAAFFPNYNNRYPQIPVQGLTREVTYDPLINFNPOLSVAQLPTFNWESSAIRNPHL 300
Db 241 DIAAFFPNYNNRYPQIPVQGLTREVTYDPLINFNPOLSVAQLPTFNWESSAIRNPHL 300
Qy 301 FDILNNLTFTDWFVSGRNFWGGRHVVISLIGGNNITSPYIGREANQBPSPRFTNGVP 360
Db 301 FDILNNLTFTDWFVSGRNFWGGRHVVISLIGGNNITSPYIGREANQBPSPRFTNGVP 360
Qy 361 FRTLSTPLRLLQOPCORHFNHNLGEGVEFTPTNSFTYGRGRTVDSLTLPEDNSVP 420
Db 361 FRTLSTPLRLLQOPWPAPPFNLRGVEGVEFTPTNSFTYGRGRTVDSLTLPEDNSVP 420
Qy 421 PREGYSRHLCHATFVQSGTPELTTGVVFSWTHRSATLNTIDPERINQIPLVKGRVWG 480
Db 421 PREGYSRHLCHATFVQSGTPELTTGVVFSWTHRSATLNTIDPERINQIPLVKGRVWG 480
Qy 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNIINSPIQRYRLFRVYASSRDARVILTGAA 540
Db 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNIINSPIQRYRLFRVYASSRDARVILTGAA 540

Qy 541 STVGQGVSVNMPLOKQMEIGENLTSTRTFRYTDPSNPFSPFRANPDIIIGISEQPLFGAGSI 600
 Db 541 STVGQGVSVNMPLOKQMEIGENLTSTRTFRYTDPSNPFSPFRANPDIIIGISEQPLFGAGSI 600
 Qy 601 SSGELYIDKIEIILADATFAESDLERAOKAVNALFTSSNOIGLTKDVTDYHIDQVSNLV 660
 Db 601 SSGELYIDKIEIILADATFAESDLERAOKAVNALFTSSNOIGLTKDVTDYHIDQVSNLV 660
 Qy 661 DCLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGWRGSTDITIQGGD 720
 Db 661 DCLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGWRGSTDITIQGGD 720
 Qy 721 DVFKNYVTLPGTVDECPYLYQKIDESKLYKAYTRYELRGYIEDSODLEIYLIAYNAKH 780
 Db 721 DVFKNYVTLPGTVDECPYLYQKIDESKLYKAYTRYELRGYIEDSODLEIYLIAYNAKH 780
 Qy 781 EIVNVPCTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
 Db 781 EIVNVPCTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 8
 AAY82401
 ID AAY82401 standard; Protein; 1189 AA.
 XX AC AAY82401;
 XX DT 27-JUN-2000 (first entry)
 XX DE Bacillus thuringiensis CryIC.499 protein SEQ ID NO:12.
 XX KW Bacillus thuringiensis; CryIC; crystal protein; insecticide; insect;
 XX KM delta-endotoxin; lepidopteran; modification; genetic engineering;
 XX KW resistance; mutant; mutagenesis.
 XX OS Bacillus thuringiensis.
 XX OS Synthetic.
 XX US56033874-A.
 XX PD 07-MAR-2000.
 XX PF 18-MAY-1999; 99US-0314093.
 XX PR 26-NOV-1997; 97US-0980071.
 XX PR 27-NOV-1996; 96US-0757536.
 XX PA (ECOG-) ECOGEN INC.
 XX PI Mettuss AL, Baum JA, Gilmer AJ;
 XX WI; 2000-255697/22.
 XX PT New mutant Bacillus thuringiensis endotoxin, used for controlling
 PT lepidopteran pests, has mutated loop region to impart higher
 PT insecticidal activity -
 XX Example 13; Column 103-106; 153pp; English.
 XX CC The present invention describes isolated Bacillus thuringiensis CryIC
 CC delta-endotoxin polypeptides having: (i) at least one amino acid (aa)
 CC mutation in the loop region between alpha-helices 6 and 7 of domain 1;
 CC and (ii) better activity against Lepidoptera than the native CryIC.
 CC The polypeptides, possibly after activation in the digestive tract of
 CC insects, kills insect cells by formation of pores and disturbing
 CC cellular homeostasis. The polypeptides are used to control lepidopteran
 CC pests on plants, either: (i) applied as a composition; or (ii) expressed
 CC in plants from heterologous nucleic acid (generating insect-resistant
 CC plants). They are more active against Lepidoptera than native CryIC.
 CC AAA08144 to AA08182, and AAY82396 to AAY82432, represent sequences used
 CC in the exemplification of the present invention.
 XX

Qy Sequence 1189 AA;
 Query Match 98.4%; Score 4289; DB 21; Length 1189;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 814; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
 Qy 1 MEENNQICIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
 Db 1 MEENNQICIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
 Qy 61 DFVWGIIVGSQMDAFLVQIQLINERIASFARNAAIANLEGLGNFNFIYVEAFKEWEDP 120
 Db 61 DFVWGIIVGSQMDAFLVQIQLINERIASFARNAAIANLEGLGNFNFIYVEAFKEWEDP 120
 Qy 121 NNPATRTVIDRPIIDGLLLEDDIPSFRIISGFEVPLLSVVAQAANLHLATLRDSVIFGER 180
 Db 121 NNPATRTVIDRPIIDGLLLEDDIPSFRIISGFEVPLLSVVAQAANLHLATLRDSVIFGER 180
 Qy 181 WGLTTINNVNENRNLIRHIDEVADHCAANTYNGLNLPKSTYQDWITYNRLRDLTLTVL 240
 Db 181 WGLTTINNVNENRNLIRHIDEVADHCAANTYNGLNLPKSTYQDWITYNRLRDLTLTVL 240
 Qy 241 DIAAEPNPNDRRYPIQPVGQLTRVYTDPLINFNPOLQSVLAQLPTFNWMESSAIRNPHL 300
 Db 241 DIAAEPNPNDRRYPIQPVGQLTRVYTDPLINFNPOLQSVLAQLPTFNWMESSAIRNPHL 300
 Qy 301 FDIANNLTFTDFWFSVGRNPFYMGHHRVVISLIGGNGITSPYIGREANQPPRSTFNPGPV 360
 Db 301 FDIANNLTFTDFWFSVGRNPFYMGHHRVVISLIGGNGITSPYIGREANQPPRSTFNPGPV 360
 Qy 361 FRTLSTPTLRLQLQPCQRHFNLRGGEVGFSTPTNSFTYRGRTGTVDSITELPPEDNSVP 420
 Db 361 FRTLSTPTLRLQLQPCQRHFNLRGGEVGFSTPTNSFTYRGRTGTVDSITELPPEDNSVP 420
 Qy 421 PREGYSHRLCHATFVQRSCTPFLTTCGVFWSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
 Db 421 PREGYSHRLCHATFVQRSCTPFLTTCGVFWSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
 Qy 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNIINSPIQRYRLFRYASSRDARVILVTGAA 540
 Db 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNIINSPIQRYRLFRYASSRDARVILVTGAA 540
 Qy 541 STVGQGVSVNMPLOKQMEIGENLTSTRTFRYTDPSNPFSPFRANPDIIIGISEQPLFGAGSI 600
 Db 541 STVGQGVSVNMPLOKQMEIGENLTSTRTFRYTDPSNPFSPFRANPDIIIGISEQPLFGAGSI 600
 Qy 601 SSGELYIDKIEIILADATFAESDLERAOKAVNALFTSSNOIGLTKDVTDYHIDQVSNLV 660
 Db 601 SSGELYIDKIEIILADATFAESDLERAOKAVNALFTSSNOIGLTKDVTDYHIDQVSNLV 660
 Qy 661 DCLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGWRGSTDITIQGGD 720
 Db 661 DCLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGWRGSTDITIQGGD 720
 Qy 721 DVFKNYVTLPGTVDECPYLYQKIDESKLYKAYTRYELRGYIEDSODLEIYLIAYNAKH 780
 Db 721 DVFKNYVTLPGTVDECPYLYQKIDESKLYKAYTRYELRGYIEDSODLEIYLIAYNAKH 780
 Qy 781 EIVNVPCTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
 Db 781 EIVNVPCTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 9
 AAE26465
 ID AAE26465 standard; Protein; 1189 AA.
 XX AC AAE26465;
 XX DT 13-DEC-2002 (first entry)
 XX DE Bacillus thuringiensis CryIC.499 mutant protein.
 XX

KW Cry1 protein; delta-endotoxin; insect resistance; lepidopteran insect;
XX transgenic plant; transgenic; mutant; mutein.
XX Bacillus thuringiensis.
OS Synthetic.
XX US6313378-B1.
XX 06-NOV-2001.
XX 21-JUN-1999; 99US-0337635.
XX 26-NOV-1997; 97US-0980071.
XX 27-NOV-1996; 96US-0757536.
XX (MONS) MONSANTO TECHNOLOGY LLC.
XX Baum JA, Gilmer AJ, Mettus AL;
XX WPI; 2002-033341/04.
XX N-PSDB; AAD44215.
XX Transgenic plants, comprises nucleic acid encoding Cry1C
PT delta-endotoxin polypeptide, has improved resistance to Lepidopteran
PT insects
XX
XX Disclosure; Column 209-216; 151pp; English.
XX
XX The present invention relates to novel transgenic plants comprising Cry1
CC delta-endotoxin genes, in particular cry1C genes that encode modified
CC crystal proteins having improved resistance to Lepidopteran insects. The
CC plants that express the mutated Cry1C delta-endotoxin crystal proteins
CC are noncoryledonous (corn, wheat, oat, rice, barley, turf grass, pasture
CC grass) or dicotyledonous (legume, soybean, cotton, fruit, berry, tree).
CC The present sequence is Bacillus thuringiensis Cry1C.499 mutant protein.
XX
XX Sequence 1189 AA;
SQ

Query Match 98.4%; Score 4289; DB 23; Length 1189;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 814; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 MEENNQCIPYNCNPNBEVLDDGERISTGNSIDISLSVQLVSNFVPGGFLVGLI 60
DB 1 MEENNQCIPYNCNPNBEVLDDGERISTGNSIDISLSVQLVSNFVPGGFLVGLI 60
QY 61 DFVWGIQVGSQWDAFLVQIEQLINERIAEFARNAATANLEGLGNFNFIYVEAFKEWEEDP 120
DB 61 DFVWGIQVGSQWDAFLVQIEQLINERIAEFARNAATANLEGLGNFNFIYVEAFKEWEEDP 120
QY 121 NNPATRTRVIDRFRILDGLLERDIPSPRISGFVEPLLSVYQAANLHLAILRDSVIFGER 180
DB 121 NNPATRTRVIDRFRILDGLLERDIPSPRISGFVEPLLSVYQAANLHLAILRDSVIFGER 180
QY 181 WGLTTINVENYNRLIRHIDEVADHCANTYNGRLNLPKSTYQDWITYNRLRDLTLVL 240
DB 181 WGLTTINVENYNRLIRHIDEVADHCANTYNGRLNLPKSTYQDWITYNRLRDLTLVL 240
QY 241 DIAAFPPNDRRYPIQVQOLTREVTYDPLINFNPOLOSVQAQLPTFNVMESAIINPHL 300
DB 241 DIAAFPPNDRRYPIQVQOLTREVTYDPLINFNPOLOSVQAQLPTFNVMESAIINPHL 300
QY 301 FDLIANNLTFTDFSVGRNPFYMGCHRVITSSLLIGCNITSPYIGREANQEPSPRSTFNGPV 360
DB 301 FDLIANNLTFTDFSVGRNPFYMGCHRVITSSLLIGCNITSPYIGREANQEPSPRSTFNGPV 360
QY 361 FRLTSLPTLLRLLQPCORHHNLRGEGVEFTPTNSFTYRGVGTVDLSLTPEDNSVP 420
DB 361 FRLTSLPTLLRLLQPCWAPPNLRGEGVEFTPTNSFTYRGVGTVDLSLTPEDNSVP 420
QY 421 PREGSHRLCHATVQVRSCTPPLTTCVVPFSTHRSATLNTDIPERINQILVKGFRVWG 480
DB 421 PREGSHRLCHATVQVRSCTPPLTTCVVPFSTHRSATLNTDIPERINQILVKGFRVWG 480

QY 481 GTSVITPGFTGGDILRENTPGDFVSLQVNIINSPIQRYRLFRFYASSRDARVIVLTGAA 540
DB 481 GTSVITPGFTGGDILRENTPGDFVSLQVNIINSPIQRYRLFRFYASSRDARVIVLTGAA 540
QY 541 STVGQGVSNMPLQKTMEIGENLTSTRFTYDFSNPFSFRANPDIIIGISEQPLFGAGSI 600
DB 541 STVGQGVSNMPLQKTMEIGENLTSTRFTYDFSNPFSFRANPDIIIGISEQPLFGAGSI 600
QY 601 SSGELYDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLTKDVTDYHIDQVSNLV 660
DB 601 SSGELYDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLTKDVTDYHIDQVSNLV 660
QY 661 DCLSDFECLDKRELSEKVKHAKLSDERNLLQDNPFRGINRQPDRCWRGSTDITIQGSD 720
DB 661 DCLSDFECLDKRELSEKVKHAKLSDERNLLQDNPFRGINRQPDRCWRGSTDITIQGSD 720
QY 721 DVFKENYVTLPGTVDECTPTLYOKIDESKLYATRYELRGYIEDSQDLIELIYLIYNAKH 780
DB 721 DVFKENYVTLPGTVDECTPTLYOKIDESKLYATRYELRGYIEDSQDLIELIYLIYNAKH 780
QY 781 EIVNVPQTGSLMPLSAQSPICKGCEPNRCAPHLEWNPDLDCSC 823
DB 781 EIVNVPQTGSLMPLSAQSPICKGCEPNRCAPHLEWNPDLDCSC 823

RESULT 10
ABG93819
ID ABG93819 standard; Protein; 1189 AA.
XX
XX ABG93819;
AC
XX
XX 26-NOV-2002 (first entry)
DT
XX
XX B. thuringiensis Cry mutant Cry1C-H121H.
DE
XX
XX Crystal protein; Cry1C; mutant; delta-endotoxin; insecticide; mutein;
KW lepidopteran insect.
XX
XX Bacillus thuringiensis.
OS
XX
XX Synthetic.
OS
XX
XX US6423828-B1.
PN
XX
XX 23-JUL-2002.
PD
XX
XX 22-JUN-1999; 99US-0337280.
PF
XX
XX 26-NOV-1997; 97US-0980071.
PR
XX
XX 27-NOV-1996; 96US-0757536.
PR
XX
XX (MONS) MONSANTO TECHNOLOGY LLC.
PA
XX
XX Baum JA, Gilmer AJ, Mettus AL;
PI
XX
XX WPI; 2002-705183/76.
DR
XX
XX N-PSDB; ABS70786.
DR
XX
XX New delta endotoxin polypeptides, which are Lepidopteran-toxic
PT polypeptides, useful as an insecticide, particularly for killing
PT Lepidopteran insects or insect cells -
PT
XX
XX Example 6; Column 101-106; 149pp; English.
PS
XX
XX The invention relates to an isolated Cry1Ca* delta-endotoxin polypeptide
CC useful as an insecticide. Cry is a crystal protein from B. thuringiensis.
CC The isolated Cry1Ca* delta-endotoxin polypeptide comprises:
CC (a) one or more amino acid mutations in the loop regions between alpha
CC helices 4 and 5 of domain 1; (b) one or more amino acid mutations in the
CC loop region between alpha helices 6 and 7 of domain 1; or (c) has
CC improved activity against Lepidopteran insects relative to a native Cry1C
CC delta-endotoxin polypeptide. The Cry1Ca* delta-endotoxin polypeptide is
CC useful as an insecticide, particularly for killing Lepidopteran insects

CC or insect cells. The present sequence represents a mutant CryIC protein
 CC of the invention.

XX SQ Sequence 1189 AA;
 Query Match 98.4%; Score 4289; DB 23; Length 1189;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 814; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MEENNQCIPNCLSNPEEVLDDGERISTGNSSIDISLSVQFLVSNFVPGGFLVGLI 60
 DB 1 MEENNQCIPNCLSNPEEVLDDGERISTGNSSIDISLSVQFLVSNFVPGGFLVGLI 60
 QY 61 DFVWGIVGSPQWDAFLVQIEQLINERIAAFARNAAIANLEGLNPNFYVEAFKWEEDP 120
 DB 61 DFVWGIVGSPQWDAFLVQIEQLINERIAAFARNAAIANLEGLNPNFYVEAFKWEEDP 120
 QY 121 NNPATRTRVIDRFRILDDGLLDRIDPSFRISGFEVPLLSVYAQAANLHLAILRDSVIFGER 180
 DB 121 NNPATRTRVIDRFRILDDGLLDRIDPSFRISGFEVPLLSVYAQAANLHLAILRDSVIFGER 180
 QY 181 WGLTTINVENNRLIRHIDEYADHCANTYRGLNLPKSTYQDMITYNLRDLTLTVL 240
 DB 181 WGLTTINVENNRLIRHIDEYADHCANTYRGLNLPKSTYQDMITYNLRDLTLTVL 240
 QY 241 DIAAFPPNDNRRYPQIPVGQLTREVYTDPLINFNPQLOSVAQLPTFNVMESSAIRNPHL 300
 DB 241 DIAAFPPNDNRRYPQIPVGQLTREVYTDPLINFNPQLOSVAQLPTFNVMESSAIRNPHL 300
 QY 301 FDILNNLTIFTDWSVGRNFGVGGHVRVSSLIIGGNITSPYIGREANQPPRSPFTNGVP 360
 DB 301 FDILNNLTIFTDWSVGRNFGVGGHVRVSSLIIGGNITSPYIGREANQPPRSPFTNGVP 360
 QY 361 FRTLSTPLRLQQPCQRHHNLRGEGVEFSTPTNSFTYRGRGTVDSTLTELPPEDNSVP 420
 DB 361 FRTLSTPLRLQQPCQRHHNLRGEGVEFSTPTNSFTYRGRGTVDSTLTELPPEDNSVP 420
 QY 421 PREGYSHRLCHATFVQRSCTPFLTTGVVFSWTHRSATLNTTIDPERINQIPLVKGFRVWG 480
 DB 421 PREGYSHRLCHATFVQRSCTPFLTTGVVFSWTHRSATLNTTIDPERINQIPLVKGFRVWG 480
 QY 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNSIPITQRYRLFRYASSDARVIVLTGAA 540
 DB 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNSIPITQRYRLFRYASSDARVIVLTGAA 540
 QY 541 STGVGQSVNMPLOKTMIEGNLTSRTRYTDFSNPPSFRANPDIIIGISEQPLFCAGSI 600
 DB 541 STGVGQSVNMPLOKTMIEGNLTSRTRYTDFSNPPSFRANPDIIIGISEQPLFCAGSI 600
 QY 601 SSGELYIDKIEIILADATPEAESDLERAQKAVNALFTSSNQIGLKTVDYDHIQVSNLV 660
 DB 601 SSGELYIDKIEIILADATPEAESDLERAQKAVNALFTSSNQIGLKTVDYDHIQVSNLV 660
 QY 661 DCLSEFCLEKREISEKVKHAKRLSDERNLLQDNFRGINQPPRGWGSTDIITIQGD 720
 DB 661 DCLSEFCLEKREISEKVKHAKRLSDERNLLQDNFRGINQPPRGWGSTDIITIQGD 720
 QY 721 DVFKNYVTLPGTVDECPTYLYQKIDESKAYTRYELRGVIEDSDQLEIYLIRYNAKH 780
 DB 721 DVFKNYVTLPGTVDECPTYLYQKIDESKAYTRYELRGVIEDSDQLEIYLIRYNAKH 780
 QY 781 EIVNVPGTGLWPLSAQSPIGKGBPNRCAPHLEWNPDLDCSC 823
 DB 781 EIVNVPGTGLWPLSAQSPIGKGBPNRCAPHLEWNPDLDCSC 823

RESULT 11

AAR39757

ID AAR39757 standard; Protein; 1189 AA.

XX AC AAR39757;

XX DT 25-MAR-2003 (updated)

DT 28-JAN-1994 (first entry)
 XX Delta endotoxin.
 XX Endotoxin; Bacillus; lice; insecticide; sheep.
 OS Bacillus thuringiensis PS81I (Clone 81IB2).
 PN WO9314641-Al.
 XX 05-AUG-1993.
 PF 31-DEC-1992; 92WO-US11337.
 PR 29-JAN-1992; 92US-0828788.
 XX (MYCO) MYCOGEN CORP.
 PA Hickie LA, Payne J;
 PI WPI; 1993-258266/32.
 DR N-PSDB; AAQ47294.
 XX Controlling biting lice on sheep - comprises administering
 PT Bacillus thuringiensis toxins to host
 PS Disclosure; Page 58-60; 64pp; English.
 XX Many strains of Bacillus thuringiensis (B.t) produce insecticidal
 CC delta endotoxins. A number of these endotoxins have been found to
 CC be toxic to Damilina ovis, the biting louse of sheep. The B.T.
 CC isolates which produce these toxins can be grown and the delta
 CC endotoxin which is produced can be recovered by standard procedures.
 CC The genes encoding these endotoxins can also be transferred to a
 CC suitable host via a recombinant vector and the resulting
 CC transformants used in methods to control lice.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 SQ Sequence 1189 AA;
 Query Match 98.4%; Score 4288; DB 14; Length 1189;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MEENNQCIPNCLSNPEEVLDDGERISTGNSSIDISLSVQFLVSNFVPGGFLVGLI 60
 DB 1 MEENNQCIPNCLSNPEEVLDDGERISTGNSSIDISLSVQFLVSNFVPGGFLVGLI 60
 QY 61 DFVWGIVGSPQWDAFLVQIEQLINERIAAFARNAAIANLEGLNPNFYVEAFKWEEDP 120
 DB 61 DFVWGIVGSPQWDAFLVQIEQLINERIAAFARNAAIANLEGLNPNFYVEAFKWEEDP 120
 QY 121 NNPATRTRVIDRFRILDDGLLDRIDPSFRISGFEVPLLSVYAQAANLHLAILRDSVIFGER 180
 DB 121 NNPATRTRVIDRFRILDDGLLDRIDPSFRISGFEVPLLSVYAQAANLHLAILRDSVIFGER 180
 QY 181 WGLTTINVENNRLIRHIDEYADHCANTYRGLNLPKSTYQDMITYNLRDLTLTVL 240
 DB 181 WGLTTINVENNRLIRHIDEYADHCANTYRGLNLPKSTYQDMITYNLRDLTLTVL 240
 QY 241 DIAAFPPNDNRRYPQIPVGQLTREVYTDPLINFNPQLOSVAQLPTFNVMESSAIRNPHL 300
 DB 241 DIAAFPPNDNRRYPQIPVGQLTREVYTDPLINFNPQLOSVAQLPTFNVMESSAIRNPHL 300
 QY 301 FDILNNLTIFTDWSVGRNFGVGGHVRVSSLIIGGNITSPYIGREANQPPRSPFTNGVP 360
 DB 301 FDILNNLTIFTDWSVGRNFGVGGHVRVSSLIIGGNITSPYIGREANQPPRSPFTNGVP 360
 QY 361 FRTLSTPLRLQQPCQRHHNLRGEGVEFSTPTNSFTYRGRGTVDSTLTELPPEDNSVP 420
 DB 361 FRTLSTPLRLQQPCQRHHNLRGEGVEFSTPTNSFTYRGRGTVDSTLTELPPEDNSVP 420
 QY 421 PREGYSHRLCHATFVQRSCTPFLTTGVVFSWTHRSATLNTTIDPERINQIPLVKGFRVWG 480

Db 421 PREGSHRLCHATFVQSGTPTLTGGVSWTHRSATLNTIDPERINQPLVKGFRVWG 480
 Qy 481 GTSVITGPTGTDILRRNTGDFVSLQVNSPTQRYRLRFYASSRDARVILTGAA 540
 Db 481 GTSVITGPTGTDILRRNTGDFVSLQVNSPTQRYRLRFYASSRDARVILTGAA 540
 Qy 541 STGVGGQVSNMPLQKTMEIGENLTSRTFYTDSPNPFSSFRANPDIIIGISEQPLFGAGSI 600
 Db 541 STGVGGQVSNMPLQKTMEIGENLTSRTFYTDSPNPFSSFRANPDIIIGISEQPLFGAGSI 600
 Qy 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLTKTDVTDYHIDQVSNLV 660
 Db 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLTKTDVTDYHIDQVSNLV 660
 Qy 661 DCLSDFECLDEKRELSEKVKHAKLSDERNLLQDPNFRGINRQPDRCWRGSTDITIQQGD 720
 Db 661 DCLSDFECLDEKRELSEKVKHAKLSDERNLLQDPNFRGINRQPDRCWRGSTDITIQQGD 720
 Qy 721 DVFKENYVTLPGTVDECYPTLYQKIDESKLYKATRYELRGYIEDSDLEIYLIYNAKH 780
 Db 721 DVFKENYVTLPGTVDECYPTLYQKIDESKLYKATRYELRGYIEDSDLEIYLIYNAKH 780
 Qy 781 EIVNVPGTGLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823
 Db 781 EIVNVPGTGLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 12

AAW61337 standard; Protein; 1189 AA.
 ID AAW61337

AC AAW61337;
 DT 30-SEP-1998 (first entry)
 XX A mutated Cry1C protein designated Cry1C-R180A.

KW Mutant; Cry1C delta-endotoxin; Cry1C-R180A; insecticidal activity;
 control; insect; Lepidoptera; Spodoptera exigua; Plutella xylostella;
 Trichoplusia ni; Spodoptera frugiperda.

XX Synthetic.
 OS Bacillus thuringiensis.

XX Key Location/Qualifiers
 XX Misc-difference 148 /label= R180A

XX WO9823641-A1.

XX 04-JUN-1998.

XX 26-NOV-1997; 97MO-US22181.

XX 27-NOV-1996; 96US-0757536.

XX (ECOG-) ECOGEN INC.

XX Baum JA, Gilmer AJ, Mettus A;

XX WPI; 1998-322660/28.

XX N-PSDB; AAV27845.

XX New Bacillus thuringiensis nucleic acid segments - comprising
 PT delta-endotoxin gene fragments, used for the control of insects,
 PT particularly Lepidopteran pests

XX Claim 1; Pages 120-122; 270pp; English.

CC The present sequence represents a mutant of the Cry1C delta-endotoxin
 CC of Bacillus thuringiensis designated Cry1C-R180A, where the Arg at
 CC position 180 of the wild type Cry1C protein is substituted with Ala.

CC The protein shows insecticidal activity, and can be sprayed onto plants
 CC or expressed in transgenic plants for the control of insects,
 CC particularly Lepidopteran pests such as Spodoptera exigua, Plutella
 CC xylostella, Trichoplusia ni and Spodoptera frugiperda.

XX Sequence 1189 AA;

Query Match 98.4%; Score 4288; DB 19; Length 1189;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MEENNQOCIPYNCNLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGLVGLI 60
 Db 1 MEENNQOCIPYNCNLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGLVGLI 60
 Qy 61 DFVWGVIPGSDWDAFLVQIEQLINERIAEFARNAALANLEGLGNFNFIYVEAFKEEEDP 120
 Db 61 DFVWGVIPGSDWDAFLVQIEQLINERIAEFARNAALANLEGLGNFNFIYVEAFKEEEDP 120
 Qy 121 NNPAITRVIDRPIILDGLLREDIPSPRISGPREVPLSVYAAANLHLAILRDSVIFGER 180
 Db 121 NNPAITRVIDRPIILDGLLREDIPSPRISGPREVPLSVYAAANLHLAILRDSVIFGER 180
 Qy 181 WGLTTINVENNLRHIDYADHCANTYNRGLANLPSKYTDQWITYNRLRDLTTLVL 240
 Db 181 WGLTTINVENNLRHIDYADHCANTYNRGLANLPSKYTDQWITYNRLRDLTTLVL 240
 Qy 241 DIAAFFPNYDNRRIPIQPVGQLTREVTYDPLINFNQLOSVAQLPTFNVMESAINPHL 300
 Db 241 DIAAFFPNYDNRRIPIQPVGQLTREVTYDPLINFNQLOSVAQLPTFNVMESAINPHL 300
 Qy 301 FDIILNLTITFTWFSVGRNFWYGGHVRVVISLIGGNITSPYVGRANQEPSPRFTENGVP 360
 Db 301 FDIILNLTITFTWFSVGRNFWYGGHVRVVISLIGGNITSPYVGRANQEPSPRFTENGVP 360
 Qy 361 FRTLSIPTLRLLQPCORHFNHNLRGEGVEFSTPTNSFTYRGRTVDSLTELPEPDSNVP 420
 Db 361 FRTLSIPTLRLLQPCORHFNHNLRGEGVEFSTPTNSFTYRGRTVDSLTELPEPDSNVP 420
 Qy 421 PREGYSHRLCHATFVQSGTPTLTGGVSWTHRSATLNTIDPERINQPLVKGFRVWG 480
 Db 421 PREGYSHRLCHATFVQSGTPTLTGGVSWTHRSATLNTIDPERINQPLVKGFRVWG 480
 Qy 481 GTSVITGPTGTDILRRNTGDFVSLQVNSPTQRYRLRFYASSRDARVILTGAA 540
 Db 481 GTSVITGPTGTDILRRNTGDFVSLQVNSPTQRYRLRFYASSRDARVILTGAA 540
 Qy 541 STGVGGQVSNMPLQKTMEIGENLTSRTFYTDSPNPFSSFRANPDIIIGISEQPLFGAGSI 600
 Db 541 STGVGGQVSNMPLQKTMEIGENLTSRTFYTDSPNPFSSFRANPDIIIGISEQPLFGAGSI 600
 Qy 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLTKTDVTDYHIDQVSNLV 660
 Db 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLTKTDVTDYHIDQVSNLV 660
 Qy 661 DCLSDFECLDEKRELSEKVKHAKLSDERNLLQDPNFRGINRQPDRCWRGSTDITIQQGD 720
 Db 661 DCLSDFECLDEKRELSEKVKHAKLSDERNLLQDPNFRGINRQPDRCWRGSTDITIQQGD 720
 Qy 721 DVFKENYVTLPGTVDECYPTLYQKIDESKLYKATRYELRGYIEDSDLEIYLIYNAKH 780
 Db 721 DVFKENYVTLPGTVDECYPTLYQKIDESKLYKATRYELRGYIEDSDLEIYLIYNAKH 780
 Qy 781 EIVNVPGTGLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823
 Db 781 EIVNVPGTGLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 13

AAW61335
 ID AAW61335 standard; Protein; 1189 AA.

XX AAW61335;

XX 30-SEP-1998 (first entry)
 XX A mutated Cry1C protein designated Cry1C-R148A.
 DE Mutant; Cry1C delta-endotoxin; Cry1C-R148A; insecticidal activity;
 KW control; insect; Lepidoptera; Spodoptera exigua; Plutella xylostella;
 KW Trichoplusia ni; Spodoptera frugiperda.
 XX Synthetic.
 OS Bacillus thuringiensis.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 148 /label= R148A
 FT
 XX W09823641-A1.
 XX
 XX 04-JUN-1998.
 XX 26-NOV-1997; 97WO-US22181.
 XX 27-NOV-1996; 96US-0757536.
 XX (ECOG-) ECOGEN INC.
 XX
 XX Baum JA, Gilmer AJ, Mettuss A;
 XX WPI; 1998-322660/28.
 XX N-PSDB; AAV27843.
 XX
 XX New Bacillus thuringiensis nucleic acid segments - comprising
 XX delta-endotoxin gene fragments, used for the control of insects,
 XX particularly Lepidopteran pests
 XX
 XX Claim 1; Pages 118-119; 270pp; English.
 XX
 XX The present sequence represents a mutant of the Cry1C delta-endotoxin
 XX of Bacillus thuringiensis designated Cry1C-R148A. The protein shows
 XX insecticidal activity, and can be sprayed onto plants or expressed in
 XX transgenic plants for the control of insects, particularly Lepidopteran
 XX pests such as Spodoptera exigua, Plutella xylostella, Trichoplusia ni
 XX and Spodoptera frugiperda.
 XX
 XX Sequence 1189 AA;
 XX
 XX Query Match 98.4%; Score 4288; DB 19; Length 1189;
 XX Best Local Similarity 98.9%; Pred. NO. 0;
 XX Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 XX
 QY 1 MEENNQNCIPYCNLSNPEVLLDGERISTGNSIDISLSVQFLVSNFVPGGFLVGLI 60
 Db 1 MEENNQNCIPYCNLSNPEVLLDGERISTGNSIDISLSVQFLVSNFVPGGFLVGLI 60
 QY 61 DFVWGIQPSQWDAFLVQIEQLINERIAEFARNAIAIANLEGNNFNIIYVEAFKWEEDP 120
 Db 61 DFVWGIQPSQWDAFLVQIEQLINERIAEFARNAIAIANLEGNNFNIIYVEAFKWEEDP 120
 QY 121 NNPAATRVIDFRILDLGLERDIPSFRISSGEVPLLSVYAAQANHLAILRDSVIFGER 180
 Db 121 NNPAATRVIDFRILDLGLERDIPSFRISSGEVPLLSVYAAQANHLAILRDSVIFGER 180
 QY 181 WGLTTINNVNENRILRHIDEYADHCANTYRGLNLLPKSTYQDWITYNRLRDLTLTVL 240
 Db 181 WGLTTINNVNENRILRHIDEYADHCANTYRGLNLLPKSTYQDWITYNRLRDLTLTVL 240
 QY 241 DIAAFPNYDNRYPQVQQLTREYVTDPLINFNPQLQSVQALPTFNVMESSAIRNPHL 300
 Db 241 DIAAFPNYDNRYPQVQQLTREYVTDPLINFNPQLQSVQALPTFNVMESSAIRNPHL 300
 QY 301 FDILNNLITFTDWFSGVGRNFYWGHRVITSSLLGGNITSPYIGREANQEPFRSFTFNGPV 360
 Db 301 FDILNNLITFTDWFSGVGRNFYWGHRVITSSLLGGNITSPYIGREANQEPFRSFTFNGPV 360

QY 361 FRTLSIPTLRLQQPCQRHHFNLRGGEVGFSTPTNSFTYRGRGTVDLSLTELPPEDNSVP 420
 Db 361 FRTLSIPTLRLQQPCQRHHFNLRGGEVGFSTPTNSFTYRGRGTVDLSLTELPPEDNSVP 420
 QY 421 PREGYSHRLCHATFVQRSCTPFLTTGCVFWSWTHRSATLTNTIDPERINQIPLVKGPRVMG 480
 Db 421 PREGYSHRLCHATFVQRSCTPFLTTGCVFWSWTHRSATLTNTIDPERINQIPLVKGPRVMG 480
 QY 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNSINSPITQRYRLFRYASSRDARVILVTGAA 540
 Db 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNSINSPITQRYRLFRYASSRDARVILVTGAA 540
 QY 541 STGVGQSVNMPLOKTMIEIGENLTSTRPTRYTDFSNPFSFRANPDIIGISEQPLFGAGSI 600
 Db 541 STGVGQSVNMPLOKTMIEIGENLTSTRPTRYTDFSNPFSFRANPDIIGISEQPLFGAGSI 600
 QY 601 SSGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKTVDVTDYHIDQVSNLV 660
 Db 601 SSGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKTVDVTDYHIDQVSNLV 660
 QY 661 DCLSDFECLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGWSGTDITIQGGD 720
 Db 661 DCLSDFECLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGWSGTDITIQGGD 720
 QY 721 DVFKENYVTLPGTVDECPYLYQKIDESKLYKAYTRYELRGYIEDSQDLEIYLIRYNAKH 780
 Db 721 DVFKENYVTLPGTVDECPYLYQKIDESKLYKAYTRYELRGYIEDSQDLEIYLIRYNAKH 780
 QY 781 EIVNVPGTGLWPLSAQSPIGKGPNCAPHLNPNPDLDCSC 823
 Db 781 EIVNVPGTGLWPLSAQSPIGKGPNCAPHLNPNPDLDCSC 823

RESULT 14

AA117790
 ID AAY17790 standard; Protein; 1189 AA.

AC AAY17790;
 AC

DT 12-AUG-1999 (first entry)
 XX

DE B. thuringiensis crystal protein Cry1C-R180A protein sequence.
 XX

KW Bacillus thuringiensis; delta-endotoxin; insecticide; crystal protein;
 KW lepidopteran insect; Cry1C; genetic engineering; mutagenesis; mutant;
 KW caterpillar; beetle; mosquito; toxic; modification.

OS Bacillus thuringiensis.
 OS Synthetic.

PN US5914318-A.
 XX

PD 22-JUN-1999.
 XX

PF 26-NOV-1997; 97US-0980071.
 XX

PR 26-NOV-1997; 97US-0980071.
 PR 27-NOV-1996; 96US-0757536.

XX (ECOG-) ECOGEN INC.
 PA

XX Baum JA, Gilmer AJ, Mettuss AL;
 PI

XX WPI; 1999-370510/31.
 DR N-PSDB; AAX80036.

XX New modified delta-endotoxin crystal proteins from Bacillus
 PT thuringiensis are useful in insecticidal compositions

XX Example 13; Column 88-90; 144pp; English.
 PS

XX The present invention describes a new composition comprising an isolated
 CC

CC polypeptide for modified Bacillus thuringiensis crystal proteins (CryIC).
 CC The polypeptide of the composition is insecticidally-active against
 CC Lepidoptera. The composition is toxic to an insect cell and comprised
 CC within an insecticidal formulation can be used as a plant protective
 CC spray which is toxic to caterpillars, beetles and mosquitoes. The
 CC polypeptide of the composition may be used to kill an insect through
 CC ingestion of the composition directly or by ingestion of a plant coated
 CC with the composition or a transgenic plant that expresses the polypeptide
 CC composition. The insecticidal proteins produced by B. thuringiensis are
 CC harmless to plants and other non-targeted organisms but toxic to their
 CC specific target insect. The polypeptides have improved toxicity so a
 CC reduced amount of bioinsecticide per unit area of treated crop can be
 CC used allowing economic and efficient utilization in the field. The
 CC present sequence represents a modified B. thuringiensis crystal protein.
 XX Sequence 1189 AA;

Query Match 98.4%; Score 4288; DB 20; Length 1189;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MEENNQCIPYCLSNPEEVLGGERISTGSSIDISLVQFLVSNFVPGGFLVGLI 60
 Db 1 MEENNQCIPYCLSNPEEVLGGERISTGSSIDISLVQFLVSNFVPGGFLVGLI 60

Qy 61 DFVNGIVGSPQMDAFLVQIEQLINERIAEFARNAATANLEGLGNFNFIYVEAFKEWEDP 120
 Db 61 DFVNGIVGSPQMDAFLVQIEQLINERIAEFARNAATANLEGLGNFNFIYVEAFKEWEDP 120

Qy 121 NNPAATRVTRIDFRILDLGLLDRIPSPRISGFEVPLLSVYQAANHLAIRDVSIFGER 180
 Db 121 NNPAATRVTRIDFRILDLGLLDRIPSPRISGFEVPLLSVYQAANHLAIRDVSIFGER 180

Qy 181 WGLTTINVENNRLIRHIDYADHCANTYNGLNLPKSTYQDWITYNRLRRDLTLVL 240
 Db 181 WGLTTINVENNRLIRHIDYADHCANTYNGLNLPKSTYQDWITYNRLRRDLTLVL 240

Qy 241 DIAAFFPNYDNRYPPIQPVGQLTREVTPLINFPQLQSVQALPTFNWESSAIRNPHL 300
 Db 241 DIAAFFPNYDNRYPPIQPVGQLTREVTPLINFPQLQSVQALPTFNWESSAIRNPHL 300

Qy 301 FDILNNLTFTDWFSGVGRNFMVGGHVRVSLIGGNTSPYIGREANQBPSPFTFNGPV 360
 Db 301 FDILNNLTFTDWFSGVGRNFMVGGHVRVSLIGGNTSPYIGREANQBPSPFTFNGPV 360

Qy 361 FRTLSIPTLLQOQCORHFNLRGGEGVEFTPTNSFTYGRGTVDLSITELPPEDNSVP 420
 Db 361 FRTLSIPTLLQOQCORHFNLRGGEGVEFTPTNSFTYGRGTVDLSITELPPEDNSVP 420

Qy 421 PREGYSRLCHATFVQSGTFFLTGTVVFSWTHRSATLTNTIDPERINQIPLVKGFRVMG 480
 Db 421 PREGYSRLCHATFVQSGTFFLTGTVVFSWTHRSATLTNTIDPERINQIPLVKGFRVMG 480

Qy 481 GTSVITGPGTGDILRRNTGDFVSLQVNNINSPTQRYRLRFYASSRDARVILTGAA 540
 Db 481 GTSVITGPGTGDILRRNTGDFVSLQVNNINSPTQRYRLRFYASSRDARVILTGAA 540

Qy 541 STGVGGQVSNMPLQKTMWIEIGENLTSTRTFYTDSPNPFSPRANPDIIIGISEQPLFGAGSI 600
 Db 541 STGVGGQVSNMPLQKTMWIEIGENLTSTRTFYTDSPNPFSPRANPDIIIGISEQPLFGAGSI 600

Qy 601 SSGELXIDKIEILLADATFEAESDLERAQKAVNALFTSSNQIGLTKTDVTDYHIDQVSNLV 660
 Db 601 SSGELXIDKIEILLADATFEAESDLERAQKAVNALFTSSNQIGLTKTDVTDYHIDQVSNLV 660

Qy 661 DCLSDFECLDKRELSEKVKHAKLSDEKNLLODPNFGINRQDRGWSGTDITIQGGD 720
 Db 661 DCLSDFECLDKRELSEKVKHAKLSDEKNLLODPNFGINRQDRGWSGTDITIQGGD 720

Qy 721 DVFKNVITLPGTVDECYPTVLYOKIDESKLYATRYELRGYIEDSDILEVILYRNAXH 780
 Db 721 DVFKNVITLPGTVDECYPTVLYOKIDESKLYATRYELRGYIEDSDILEVILYRNAXH 780

Qy 781 EIVNVPGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823
 Db 781 EIVNVPGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 15

AAAY17788 standard; Protein; 1189 AA.

XX AAAY17788;
 XX 12-AUG-1999 (first entry)
 DT B. thuringiensis crystal protein CryIC-R148A protein sequence.
 DE
 XX

XX Bacillus thuringiensis.
 XX Synthetic.
 OS
 XX US5914318-A.
 FN
 XX 22-JUN-1999.
 -PD
 XX 26-NOV-1997; 97US-0980071.
 PF
 XX 26-NOV-1997; 97US-0980071.
 PR
 XX 27-NOV-1996; 96US-0757536.
 XX (BCOG-) ECOGEN INC.
 PA

XX Baum JA, Gilmer AJ, Mettuss AL;
 PI
 XX WPI: 1999-370510/31.
 DR
 XX N-PSDB; AAX80019.

PT New modified delta-endotoxin crystal proteins from Bacillus
 thuringiensis are useful in insecticidal compositions

XX Example 5; Column 83-85; 144pp; English.

XX The present invention describes a new composition comprising an isolated
 polypeptide for modified Bacillus thuringiensis crystal proteins (CryIC).
 CC The polypeptide of the composition is insecticidally-active against
 CC Lepidoptera. The composition is toxic to an insect cell and comprised
 CC within an insecticidal formulation can be used as a plant protective
 CC spray which is toxic to caterpillars, beetles and mosquitoes. The
 CC polypeptide of the composition may be used to kill an insect through
 CC ingestion of the composition directly or by ingestion of a plant coated
 CC with the composition or a transgenic plant that expresses the polypeptide
 CC composition. The insecticidal proteins produced by B. thuringiensis are
 CC harmless to plants and other non-targeted organisms but toxic to their
 CC specific target insect. The polypeptides have improved toxicity so a
 CC reduced amount of bioinsecticide per unit area of treated crop can be
 CC used allowing economic and efficient utilization in the field. The
 CC present sequence represents a modified B. thuringiensis crystal protein.

XX Sequence 1189 AA;

Query Match 98.4%; Score 4288; DB 20; Length 1189;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MEENNQCIPYCLSNPEEVLGGERISTGSSIDISLVQFLVSNFVPGGFLVGLI 60
 Db 1 MEENNQCIPYCLSNPEEVLGGERISTGSSIDISLVQFLVSNFVPGGFLVGLI 60

Qy 61 DFVNGIVGSPQMDAFLVQIEQLINERIAEFARNAATANLEGLGNFNFIYVEAFKEWEDP 120
 Db 61 DFVNGIVGSPQMDAFLVQIEQLINERIAEFARNAATANLEGLGNFNFIYVEAFKEWEDP 120

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